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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:57:11 ; Search time 107 seconds
(without alignments)
4944.088 Million cell updates/sec

Title: US-09-623-034-1
Perfect score: 1725
Sequence: 1 tatatacacatagtctca.....gagcaaaagacttggtata 1725

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2-6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2-6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2-6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2-6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2-6/ptodata/2/ina/PCUTUS_COMB.seq:*
6: /cgn2-6/ptodata/2/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	552	32.0	1544	2	US-08-837-593-1	Sequence 1, Appl1	
	2	233	13.5	1467	1	US-08-176-620A-3	Sequence 3, Appl1	
	3	233	13.5	1467	1	US-08-463-862-3	Sequence 3, Appl1	
	4	233	13.5	1467	2	US-08-461-985-3	Sequence 3, Appl1	
	5	233	13.5	1467	2	US-08-458-887-3	Sequence 3, Appl1	
	6	233	13.5	1467	4	US-08-932-787B-3	Sequence 3, Appl1	
	7	233	13.5	1467	4	US-08-932-012C-3	Sequence 3, Appl1	
	8	233	13.5	1467	4	US-08-888-818C-3	Sequence 3, Appl1	
	9	232	13.4	1100	2	US-08-950-449A-18	Sequence 18, Appl1	
	10	232	13.4	3774	2	US-08-950-449A-11	Sequence 11, Appl1	
	11	232	13.4	3813	1	US-08-469-421-11	Sequence 11, Appl1	
	12	232	13.4	3813	1	US-08-250-975-11	Sequence 11, Appl1	
	13	232	13.4	3813	2	US-08-605-002A-11	Sequence 11, Appl1	
	14	232	13.4	3813	4	US-08-943-353-11	Sequence 11, Appl1	
	15	232	13.4	3813	5	PCT-US94-10529-11	Sequence 11, Appl1	
	16	230.4	13.4	1381	2	US-08-950-449A-13	Sequence 13, Appl1	
	17	230.4	13.4	1423	1	US-08-469-421-13	Sequence 13, Appl1	
	18	230.4	13.4	1423	1	US-08-250-975-13	Sequence 13, Appl1	
	19	230.4	13.4	1423	2	US-08-605-002A-13	Sequence 13, Appl1	
	20	230.4	13.4	1423	4	US-08-943-353-13	Sequence 13, Appl1	
	21	230.4	13.4	1423	5	PCT-US94-10529-13	Sequence 13, Appl1	
	22	230.4	13.4	1539	3	US-09-286-904-1	Sequence 1, Appl1	
	23	230.4	13.4	1539	4	US-09-640-101-1	Sequence 1, Appl1	
	24	222.2	12.9	1611	3	US-08-909-742-2	Sequence 2, Appl1	
	25	222.2	12.9	1611	4	US-09-412-289-2	Sequence 2, Appl1	
	26	220.8	12.8	3132	3	US-09-286-904-45	Sequence 45, Appl1	
	27	220.8	12.8	3132	4	US-09-640-101-45	Sequence 45, Appl1	

28	212.2	12.3	2624	1	US-08-032-382B-1	Sequence 1, Appl
29	209.4	12.1	1747	1	US-08-176-620A-1	Sequence 1, Appl
30	209.4	12.1	1747	1	US-08-463-862-1	Sequence 1, Appl
31	209.4	12.1	1747	2	US-08-461-985-1	Sequence 1, Appl
32	209.4	12.1	1747	2	US-08-458-887-1	Sequence 1, Appl
33	209.4	12.1	1747	4	US-08-932-787B-1	Sequence 1, Appl
34	209.4	12.1	1747	4	US-08-932-012C-1	Sequence 1, Appl
35	209.4	12.1	1747	4	US-08-888-818C-1	Sequence 1, Appl
36	209.4	12.1	1866	3	US-08-909-742-1	Sequence 1, Appl
37	209.4	12.1	1866	4	US-09-412-289-1	Sequence 1, Appl
38	185.4	10.7	1023	3	US-08-554-385-4	Sequence 4, Appl
39	183.8	10.7	1200	1	US-08-011-398B-3	Sequence 3, Appl
40	183.8	10.7	1200	1	US-08-464-051-3	Sequence 3, Appl
41	183.8	10.7	1200	2	US-08-462-498-3	Sequence 3, Appl
42	170.2	9.9	1851	1	US-08-674-612-1	Sequence 1, Appl
43	170.2	9.9	1851	1	US-08-700-575-45	Sequence 1, Appl
44	170.2	9.9	1851	2	US-08-920-296-1	Sequence 1, Appl
45	170.2	9.9	1851	4	US-09-124-163-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-837-593-1
Sequence 1, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.
APPLICANT: Zhang Zhuqun
TITLE OF INVENTION: "NO. 5977442el Salicylic Acid Induced
TITLE OF INVENTION: Map kinase and its use for Enhanced Disease Resistance in p
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESSER: P. C.
STREET: 1601 Market Street, Suite 720
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1544 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE: tobacco
US-08-837-593-1

MOLECULE LIFE: DNA (genomic)

Oy 1206 CAGGAAGCTTTGTACATGATCCTGAATA 1234
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Db 1210 GAAGAGACTGCTCGATTCCAGCAGAGATA 1238

RESULT 5
US-08-458-887-3

: Sequence 3, Application US/08458887
: Patent No. 5914261
: GENERAL INFORMATION:
: APPLICANT: Boulton, Teri G. et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,887
: FILING DATE: 02-JUN-1995
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/701,544
: FILING DATE: 16-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Mistrock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 6526-049
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1467 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: unknown
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1245
: US-08-458-887-3

Query Match 13.5%; Score 233; DB 2; Length 1467;
Best Local Similarity 55.2%; Pred. No. 7.3e-55;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps 4;

Oy 258 ATTGCTGCTGCTGCTTATGAAATGTCGCTCCGCTTGATFACGAGAGCTGAATGATG 317
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Db 256 ATCGGAGAGGCGCTACGGATGCTGTTGCTGCTTATGATATCTCAACAAAGTTGCA 315
Oy 318 GTTCAGATTAGAAAATCGCAATGCGTTTGATATTACATGATGCTAAGAGACTCTC 377
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Db 316 GTTGCTATCAAGAAATC---AGTCCTTTGAGCACCGACTACTGTCAAGAAACCTG 372
Oy 378 CGTAGATTAAAGTCCTCCGCCATTTAGACCATGAATAATGATTGTTAAGACAGCTG 437
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Db 373 AGAAGATATAAATCTACTCGCTTCAGACATGAGAACATCATCGCATCAATGACATC 432
Oy 438 ATTCCTCCACCCTTACGAAGAGATTTCTGATGTTTACATTTGCTACTGAAGACTGAT 497
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Db 433 ATCGGGGCGCAACCATTTGACAGATGAATAATGATATATATAGTACAGACTTGGAG 492
Oy 498 ACTGATCTTCACCAATATATAGATCCAAAGGTTTATGAGAGATCACTGTGATGAC 557

Db 493 ACAGATCTTTACAAAGCTTTGAGAGACAGACA-----CTCAGCAATGATCATATCTGCTAT 549
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Oy 558 TTCAATGATACAGTCTCCGCTGCTGCTTAAATACATACATCCGCAATGTTCTTCAATAGA 617
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Db 550 TTTCTTTATCAGATCTCAGAGAGATTAAAGTATATACATTCAGCTAAATGTTGACCGGT 609
Oy 618 GATCTCAACCGGACCAACCTTTTGTAAATGCAAAATTTGATCTTAAGATATGTGACTTT 677
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Db 610 GAACCTCAAGCCCTCCAACTCCCTGCTGAACACACCTTGTGATCTCAACATCTGACACTT 669
Oy 678 GATCTTGC---TAGGCCAATAGAGAAAGAGAATA-----TGACGGAATATGTT 725
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Db 670 GGCCTTGCCCGGTGTTCAGATCCAGACCATATCATATACAGGTTCTTGACAGAGATGTA 729
Oy 726 GTAACCATGATGTACAGGCGACACAGAGCTTTGTGAACCTTTCAGATATACATGCTGCT 785
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Db 730 GCCACGCGTGTGTACAGAGCTCCAGAAATATGTTGAATTCCAAGGGTTATACCAAGTCC 789
Oy 786 ATAGATGTTTGTCTGTGGTGTGATCTTTCATGGAACCTATGAATAGAAAACCTTTGTT 845
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Db 790 ATTGATATTGCTGTGTGGCTGCATCTGCGAGAGATGCTATCCAAAGCCCTATCTTC 849
Oy 846 GATGGAATAAGATCATGTACATCAATAACGCTTTGTTAACCGAGCTTCTGGCACCCACACA 905
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Db 850 CCAGGAAGCATTTACCTTGACCGACTGAATCACAATCCTGGGTATTTCTGATCTGCATCA 909
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Db 970 CACAAAATTAAGTGCCTGTGAACAGTTGTTCCAAAACGCTGACTCCAAAGCTCTGGAT 1029
Oy 1026 CTTCGATTAATAATGTTGACATTCGATCTACTAGAAATTAAGATAGAGAAACATTA 1085
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Db 1030 TTACTGATTAATAATGTTGACATTTTAACCTCACAAGAGATTTGAAGTTGAACAGCTGTG 1089
Oy 1086 GATCATCCCTACCTTGCAAGAGCTCCAGATGAGGTGAGCAACCGATGCTCCCTGTCCA 1145
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Db 1090 GCCCACCCGTACTCGAGACAGTATTTATGACCAAGTATGAGCCCATTTGCTGAAGCACCA 1149
Oy 1146 TTCTCCTTTGACTTGGACCAAGGAATAGAGAAAGCAAAATTAAGCATGATATAT 1205
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Db 1150 TTCAAGTTTGAATGAGAGCTGAGACTTACCTTAAGGAAGCTCAAGAACTCATTTT 1209

Query Match 12.0%; Score 233; DB 2; Length 1467;
Best Local Similarity 55.2%; Pred. No. 7.3e-55;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps 4;

Oy 1206 CAGGAAGCTTTGTACATGATCCTGAATA 1234
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Db 1210 GAAGAGACTGCTCGATTCCAGCAGAGATA 1238

RESULT 6
US-08-932-787B-3
: Sequence 3, Application US/08932787B
: Patent No. 6277963
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: ANTIBODIES DIRECTED TOWARD EXTRACELLULAR SIGNAL-RELATED
: FILE REFERENCE: REG 430-A-1
: CURRENT APPLICATION NUMBER: US/08/932,787B
: CURRENT FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 08/469,547
: PRIOR FILING DATE: 1995-06-06
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0

Db	670	GGCCTTGCCCGTGTGGCAGATCCAGACCATGATCATACAGGGTCTTGCACGATGATSTA	729
Qy	726	GTAAACAGATGTAACAGGGCACCAGAGCTTTTGTGAACTCTTCAGATTACACTGCTCT	785
Db	730	GCCACGGSTGTGTACAGAGCTCCAGAAATTATGTTAAATTCAGAGGTTATATCCAAAGCC	789
Qy	786	ATATATGTTTGGTCTGTGCGGTTGCTATCTTCATGAACTTATCAATAGAAAACCTTTGTT	845
Db	790	ATTATATTGGTGCTGTGGGCTGCATCTCGCAGAGATGCTATCCAGAGGCTATCTTC	849
Qy	846	GGTGGAAAAATCATGTATGATCAATCAAAATACGTTGTTAACGACCTTGTGGACCCCAACA	905
Db	850	CCAGGAAAGCATTAACCTTGACACGCTGAAATCACATCTGGTATTTCTTGATCTTCATCA	909
Qy	906	GAACTGATCTTGGCTTCTCCAAAATGGAAGATGCAAGAGATACATGAGCAACTCCCA	965
Db	910	CAGGAAATCTGATTTGATTTATATATTAATTTAAAAAGTAGAAATATTTGCTTCTCTCCG	969
Qy	966	CAACATCTCGCCGACGAGTTAGCAGAAAGTTTCCCATGTAACCCATTTGGCTTTGAT	1025
Db	970	CACAAAAATAAGTGCGCCGTGGAACAGGTTGTTCCCAACGCTGACTCCAAAGCTTGAT	1029
Qy	1026	CTTGTGATAAAAATGTTGACATTCGATCTCTACTAGAAAGATTACAGTTGAGGAACATTA	1085
Db	1030	TTACTGATTAATAATGTTGACATTTTAACCCGCAAGAGAGATTGAAGTTGAACAGGCTGTG	1089
Qy	1086	GATATATCCCTACCTTGCAAAAGCTCCACAGATGCAAGGTGACGAACGATCTGCCCTGTCCA	1145
Db	1090	GCCACCCGAGCTCGGAGCGATTTATGTGACCCCAAGGATGAGACCCATTGCTCAACACACA	1149
Qy	1146	TTTCTCTTACATTTTGACGAAACAGGAAATAGGAGAAACAATTAAGACATGATATAT	1205
Db	1150	TTCAAGTTTACATGAGAGCTGAGACGACATTAACCTAAGAGAAACCTCAAAAGACTATTTT	1209
Qy	1206	CAGGAAGCTTTGTACTGAAATCCTGATA	1234
Db	1210	GAAAGACTGCTGATTTCCAGCCAGGATA	1238

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RESULT
US-08-888-818C-3
: Sequence 3, Application US/08888818C
: Patent No. 630358
: GENERAL INFORMATION:
: APPLICANT: Boulton et al.
: TITLE OF INVENTION: A FAMILY OF MAP2 PROT
: FILE REFERENCE: REG 430-V-1
: CURRENT APPLICATION NUMBER: US/08/888,818C
: PRIOR FILING DATE: 1997-07-07
: PRIOR APPLICATION NUMBER: 08/478,985
: PRIOR FILING DATE: 1995-06-07
: PRIOR APPLICATION NUMBER: 08/178,488
: PRIOR FILING DATE: 1994-01-07
: PRIOR APPLICATION NUMBER: 07/701,544
: PRIOR FILING DATE: 1991-05-16
: PRIOR APPLICATION NUMBER: 07/532,004
: PRIOR FILING DATE: 1990-06-01
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 1467
: TYPE: DNA
: ORGANISM: RAT
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1245)
: OTHER INFORMATION: ERK2 cDNA
: US-08-888-818C-3

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Query Match	13.58;	Score 233;	DB 4;	Length 1467;
Best Local Similarity	55.28;	Pred. No. 7.3e-55;		
Matches 546;	Conservative 0;	Mismatches 425;	Indels 18;	Gaps 4;

QY	258	ATTGTCGTGTCGTTATGCAATTTGTCGTGCGGTGTTGAATACGAGCTGATATGATG	317
Db	256	ATCGAAGAAAGCGCCCTCGGCGATGCGTTGTTCGCTTAATGATTAATCTCAACAAAGTTGGA	315
QY	318	GTTGAGATTAAAGAAATACGGGAATGCGTTGATTAATTAATGATGATCGTAAGAGACTGTC	377
Db	316	GTTGCTATCAAGAAAATC---AGTCCTTTTGAGACACCAGACCTACTGTAGAGAACCTTG	372
QY	378	CGTGAATTAAAGCTCCTCCGCCATTTTAAAGACGAAATGTAAATGGTTTAAAGAGACGTG	437
Db	373	AGAGAGATAAAAATCCTACTGCGGCTTCAGACATGAGAACATCATGGCATCAATGACATC	432
QY	438	ATTCTCCACCCCTTACGAAAGGAGTTTTCGATGTTTACATTTGCTACTGAACTCATGAT	497
Db	433	ATCCGGGACCAACCATTTGACAGATGAAGATGAATATATATAGTACAGGACCTCTAGAG	492
QY	498	ACTGATCTTCCAAATATATTAATCCACCAAGTTTATTCAGAGATGACTGTAGTAC	557
Db	493	ACAGATCTTTACAAGCTCTTGAAGACACACA---CCTGAGCAATGATATATCTGCTAT	549
QY	558	TTTCATGTATACGCTCTCCGTGGCCTTAATATACATACATTCGCGCAATGTTCTTATGCA	617
Db	550	TTTCTTATACAGATCCCTGAGAGGATTAAGATATATACATTCAGCTAATGTTCTGCACGT	609
QY	618	GATCCCAACCGACACACTTTTGGTAAATGCAAAATTTGATCTTAAATATGACTTT	677
Db	610	GACCTCAAGCCTTCCAAACCTCTGCTGTAACACACACTTGTGATCTCAAGTCTGTACTTT	669
QY	678	GGTCTTGC--TAGGCCAAACATAGAGAACGAGATA-----TGACGGAATATGTT	725
Db	670	GGCCTCGCCCGTGTGGCAGATCCAGACCATGATCATACAGGGTCTTGACAGATGTA	729
QY	726	GTAACCAAGTGTACAGGACACAGACGCTTTGTAACTCTTCAGATTAACACTGCTCT	785
Db	730	GCCACGGGTGTGTAACAGCTCCAGAAATATTTTAATTTCCAAAGGTTATACCAAGTCC	789
QY	786	ATATAGTTTGGTCTGTCGGTGTGCATCTTCATGGAAGCTATGAAATAGAAACCTTTGTTT	845
Db	790	ATTGATATTTGGTCTGTGGGCTGCATCTGTGCGAGATGCTATCCAAACGCGCTATCTTC	849
QY	846	GGTGGAAAAATCATGTACATCAAATACGCTTGTAAACGACCTTCTTGGCACCCCAACA	905
Db	850	CCAGAAAGCAATTCCTTGGACCGAGTAATCATCATCTCGGATATCTTGGATCTCATCA	909
QY	906	GAAGCTATCTGGCTTCCTCCAAATGGAAGATGCAAAAGATACATCAGCAATCCCA	965
Db	910	CAGAAAGTCTGAATTTATTAATTAATTTAAAGCTAGAAACTATTTGCTTCTCTCCG	969
QY	966	CAACATCCTCGCGACAGTTAGAGAAAGTTTCCCTCATGTGAACCCATTTGGCTTTGAT	1025
Db	970	CACAAAATATAGTGGCGGTGGAACAGTTGTTCCCAACGCTGACTCCAAAGCTTGAT	1029
QY	1026	CTTGCTGATTAATATGTTGACATTCGATCCTACTAGAAGATTTACAGTTGAGGAACATTA	1085
Db	1030	TTACTGATTAATAATGTTGACATTTTAAACCTCCACAAAGAGATTTGAATGAACAGCTCG	1089
QY	1086	GATATCCCTACCTGTGCAAGCTCCACAGATGCAAGGTGAGCAAGCATCTGCCCTGTCCA	1145
Db	1090	GCCACCCGTCCTCGGAGCAGTATTATGACCCCAAGGATGAGCCCATTTGCTGAAACACCA	1149
QY	1146	TTTCCTCTTGACTTTGAGCAACAAGAAATAGGAAGACCAATTTAAGACATGATATAT	1205
Db	1150	TTTCAAGTTTGACATGAGAGCTGGAACGACTTACCTTAAGAGAAAGCTCAAGAACTATTTT	1209
QY	1206	CAGAGACCTTTTGTACTGAATCTCTGAATA	1234
Db	1210	GAAAGACTGCTGATTTCCAGCCAGGATA	1238

RESULT 9
US-08-950-449A-18
; Sequence 18, Application US/08950449A

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? Patent No. 5955366
? GENERAL INFORMATION:
? APPLICANT: Lee, John C.
? APPLICANT: Adams, Jerry L.
? APPLICANT: Gallagher, Timothy F.
? APPLICANT: Green, David W.
? APPLICANT: Heys, J. Richard
? APPLICANT: McDonnell, Peter
? APPLICANT: McNulty, Dean E.
? APPLICANT: Strickler, James E.
? APPLICANT: Young, Peter R.
? TITLE OF INVENTION: Drug Binding Protein
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: Corporate Intellectual Property/P.O. Box
? STREET: 1539
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/950,449A
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/123,175
? FILING DATE: 17-SEP-1993
? ATTORNEY/AGENT INFORMATION:
? NAME: Hecht, Elizabeth J.
? REGISTRATION NUMBER: P-41,824
? REFERENCE/DOCKET NUMBER: P50195-1D1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (610) 270-5009
? TELEFAX: (610) 270-5090
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1100 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? MOLECULE TYPE: linear
? TOPOLOGY: linear
? MOLECULE TYPE: CDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? US-08-950-449A-18

Query Match 13.4%; Score 232; DB 2; Length 1100;
Best Local Similarity 56.5%; Pred. No. 1.2e-54;
Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;

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Db 336 ATGGGGGAGATCTGAACAACTTGTGAAT---GTCGAAGCTTACAGATGACCATGTT 392
Qy 552 CAGTACTTCATGTATGAGCTCCCGGGGCTAAATATACATATCCGGGAATGCTCT 611
Db 393 CAGTCTTATCTACCAAAATTTCTCGAGGCTTAAAGTATATATACCTAGCATATATT 452
Qy 612 CATAGAGATCTCAACCGAGCAACCTTTGGTAAATGCAATTGTGATCTTAAAGATATGT 671
Db 453 CACAGGAGCCTAAACCTAGTAATCTAGTGAATGAAGACTGTGAGCGAAGATCTGT 512
Qy 672 GACTTTGCTGTCTAGGCCAAACATAGACAGACAGATATGACGGAATATGTTTGAAC 731
Db 513 GATTTGGAGCTGGCTCGCACA-----CAGATGATAAATGACAGGCTGGCGCACT 566
Qy 732 AGATGTACAGAGGACAGACCTTTGTTGTAACCTTCAGATTCAGTCTGCTATATAGAT 791
Db 567 AGTGATACAGAGGCTCCTGAGATCATCTGACACTGATGATTTCAACAGACAGTGTAT 626
Qy 792 GTTTGGTCTGTGGTTCATCTTCATGAACTTATGAAATGAAAACTTTGTTGGTGA 851
Db 627 ATTTGGTCAGTGGGATCATATATGCGCAGCTGTGACTGGAAACATTTGTTCCGTGT 686
Qy 852 AAAGATCATGATCAATCAATATAGCTGTTAACGAGAGCTTCTGGCACCACCAAGAGCT 911
Db 687 ACAGACCATATTTAACAGCTTCACAGACATTTATGCTGTGACAGAGAACACCCCGCTTAT 746
Qy 912 GATCTTGCTCTCCCAAAATGAAAGATGCAAGATACATCAGGCAACTCCCAACAT 971
Db 747 CTCATTTAACAGAGATGCCAGAGCATGAGCAAGAAATATATGCTTTGAGTCAGATG 806
Qy 972 CCTCGCCAGAGATGAGAGAGTTTCCCTCAGTATGAGTGAACCATTTGCTATGATCTGTC 1031
Db 807 CCGAAGATGAACTTTGGCAATGTATTTATGTCGCATCCCGGCTGTCGACTGCTG 866
Qy 1032 GATAAATGTTGACATTCGATCTCCTACTAGAAAGATTAAGTACAGTGGAGGATTAAGATCAT 1091
Db 867 GAGAGAGATCTCTGATTTGAGACTCAGATTAAGAAATTTACAGCGGCCCAAGCCCTTGACAT 926
Qy 1092 CCTACCTTGCMAAGCTCCACAGATGACAGGTGACGAAAC 1129
Db 927 GCTACTTGTGTGCTAGTACACAGATCTGATGATGAAC 964

RESULT 10
US-08-950-449A-11
? Sequence 11, Application US/08950449A
? Patent No. 5955366
? GENERAL INFORMATION:
? APPLICANT: Lee, John C.
? APPLICANT: Adams, Jerry L.
? APPLICANT: Gallagher, Timothy F.
? APPLICANT: Green, David W.
? APPLICANT: Heys, J. Richard
? APPLICANT: McDonnell, Peter
? APPLICANT: McNulty, Dean E.
? APPLICANT: Strickler, James E.
? APPLICANT: Young, Peter R.
? TITLE OF INVENTION: Drug Binding Protein
? NUMBER OF SEQUENCES: 19
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: Corporate Intellectual Property/P.O. Box
? STREET: 1539
? CITY: King of Prussia
? STATE: PA
? COUNTRY: USA
? ZIP: 19406-0939
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/950,449A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,175
FILING DATE: 17-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hecht, Elizabeth J.
REGISTRATION NUMBER: P-41,824
REFERENCE/DOCKET NUMBER: P50195-1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5009
TELEFAX: (610) 270-5090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 3774 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: Monocyte
FEATURE:
NAME/KEY: CDS
LOCATION: 379..1461
US-08-950-449A-11

Query Match 13.4%; Score 232; DB 2; Length 3774;
Best Local Similarity 56.5%; Pred. No. 2,2e-54;

Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;

QY 255 CCTATTGCTGCTGCTTATGAAATGCTGCTGCTGTTGAATACGAGAGCTAATGAG 314
DB 447 CCAATGGCGCTCTGGCGCTATGCTGTGCTGCTCTTTGACACAAAACGGGGTTA 506
QY 315 ATGTTGAGTTAAGAAATGCCAATCGTTTGATATTACATGAGATCTAAGAGACT 374
DB 507 CGTGGGAGTGAAGAACTCTCCAGACCATTTGATCATTCATTCAGCGAAAGAAC 566
QY 375 CTCCTGAGATTAACTCCCGCATTTAGACATGAATAATGTAATGTTAAGAGAC 434
DB 567 TACAGAGACTGCGGTACTTAACATATGAACATGAATAATGATGGTCTGTGGAC 626
QY 435 GTGATTT--CCTCCACCCTTACGAAGGAGTTTCTGATGTTTACATTTGCTACTGA 491
DB 627 GTTTTACACCTGCAAGGTCTCTGAGAGATTCATGATGTAATCTGCTGACCCATCTC 686
QY 492 ATGATATGATCTTCACCAATATATGATCCAAACCAAGTTTATCAGAGATCACTGT 551
DB 687 ATGGGGGAGATGTAACAACATTTGTGAAT--GTCAAGACCTTACAGATGACCATGTT 743
QY 552 CAGTACTTATGATACAGCTCTCCGTGGCTAAATATACATATTCGCGAATGTTCTT 611
DB 744 CAGTTCTTATCTACCAAAATCTCCGAGTCTAAAGTATATACATTCAGCTGACATAT 803
QY 612 CATGAGATCTCAACCGAGCAACCTTTGGTAAATGCAAAATGATCTTAAGATATGT 671
DB 804 CACAGGGACCTAAACACTGAATCTGATCTGAATGAAGACTGAGCTGAAGATTTGTG 863
QY 672 GACTTGTGCTGTAGGCAACATAGAGAACGAGATATGAGGAATATGTTTAAC 731
DB 864 GATTTGACTGCTCGGACACA-----CAGATGATGAATAAGACAGGCTAGCGCCACT 917
QY 732 AGATGACAGACGACAGACCTTTTGTGAACCTTTCAGATTCACAGCTGCTATAGAT 791
DB 918 AGGTGATACAGAGGCTCGTGAATCATGCTGAACAGATGATTCACACACAGATGAT 977
QY 792 GTTGGTCTGCGGTGATCTTATGAGAACTTATGAATAGAAAACCTTTGTTGGTGA 851
DB 978 ATTGTGATGAGGATGATGAATGAGCGAGCTGTGACTGGAAGAACATGTTTCTCTGT 1037

QY 852 AAGATCATGTACATCAATAATACGCTTTTAACGAGCTTCTTGACACCCCAACAGAGCT 911
DB 1038 ACAGACCAATATTAAACAGCTTCAGAGATTATGCGTCTGACAGAAACCCCTTAT 1097
QY 912 GATCTTGCTTCCCTCAAAATGAAGATGCAAGAGATACATGAGCAACTCCCAACAT 971
DB 1098 CTCATTACAGAGATGCAAGCATGAGGCAAGAACTATATTCATCTTTGACTGAGATG 1157
QY 972 CCTGCCACGACCTAGCAGAACTTTCCCTCATGTGAACCCATGCTATTGATCTTGTC 1031
DB 1158 CCGAAGATGAACCTTTGCGAATGATTTATTTGTCGCAATCCCTGCTGTGCACTTGCTG 1217
QY 1032 GATAAATGTTACATTTGATCTCTACTAGAACAAATTAAGAGTGAAGAAACATTAATCAT 1091
DB 1218 GAGAAGATGCTGTATTTGAGATCAGATTAAGAGAAATTAACAGCGGCCCAAGCCCTTGACAT 1277
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DB 1278 GCCTACTTTGCTCAGTACCAGATCTCTGATGATGAACC 1315

RESULT 11
US-08-469-421-11

Sequence 11, Application US/08469421
Patent No.5777097

GENERAL INFORMATION:

APPLICANT: Lee, John C.
APPLICANT: Adams, Jerry L.
APPLICANT: Gallagher, Timothy F.
APPLICANT: Green, David W.
APPLICANT: Heys, J. Richard
APPLICANT: McDonnell, Peter
APPLICANT: McNulty, Dean E.
APPLICANT: Strickler, James E.
APPLICANT: Young, Peter R.
TITLE OF INVENTION: Drug Binding Protein
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
STREET: Corporate Intellectual Property/ P.O. Box
STREET: 1539
CITY: King of Prussia
STATE: PA

COUNTRY: USA

ZIP: 19406-0939

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,421

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/250,975

FILING DATE: 31-MAY-1994

APPLICATION NUMBER: US 08/123,175

FILING DATE: 17-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Jervis, Herbert H.

REGISTRATION NUMBER: 31,171

REFERENCE/DOCKET NUMBER: P50195-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (610) 270-5090

TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 3813 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear


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Db 523 CGTGTGGCAGTGAAGACGCTCTCCAGACATTTGAGTCATTCATGCGGAAGAAC 582
Qy 375 CTCCTGAGATTAGCTCTCCGCCATTTAGACCATGAAATGTATTGGTTAAGAGAC 434
Db 583 TACAGAGAACTCGGCTTACTTAACATATGAACATGAATAATGTATTGCTGTGGAC 642
Qy 435 GTGATT---CCTCCACCCCTTAGAAGAGATTTTCTGATGTTTACATTGCTACTGAC 491
Db 643 GTTTTACACCTGCAAGGCTCTCTGAGGAATTCATGATGTATCTGTGTCACCATCTC 702
Qy 492 ATGATAGTATGATCTTCCACCAATAATATTAGATCAACCAAGTTTATCAGAGATCACTGT 551
Db 703 ATGGGGGAGATCTCAACAATTTGTGAAT---GTCAAGACTTACAGATACCATGTT 759
Qy 552 CAGTACTTATGATATCAGCTCCTCCGTGGCTTAAATACATACATTTCCGGAATGTTCTT 611
Db 760 CAGTCCCTTATCTACCAAAATTCCTCGAGGTCTAAAGTATATACATTACGCTGACATTAAT 819
Qy 612 CATAGAGATCTCAACCGAGACCTTTTGGTAATGCAATTTGATCTTAAGATATGT 671
Db 820 CACAGGACCTTAAACCTAGTATCTAGCTGTGAATGAAGACTGTGACCTGAAGATTCTG 879
Qy 672 GACTTTGGCTTGTAGTGGCAAAACATAGAGAAGCAATATGACGGAATATGTTGTAAC 731
Db 880 GATTTTGACCTGGCTCGGCACA-----CAGATGATGAATGACAGCTAGCTGGCCACT 933
Qy 732 AGATGTACAGGCGACACAGACCTTTGTTGAATCTTCAGATTACAGTGGCTATAGAT 791
Db 934 AGGTGTACAGGCGCTCTGAGATCATGCTGAACCTGATGATACACAGACAGCTGAT 993
Qy 792 GTTTGGTGTGGTTGATCTTCAATGACTTATGAACTTATGAAACCTTTGTTGGTGA 851
Db 994 ATTTGATAGTGGATGTGATATAGGCCAGAGCTGTGACTGGAGAATGTTGTTCTGCT 1053
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Db 1054 ACAGACCATATTTAACACACTTCAGACATTTATGCGTGTACAGAGAAACCCCCGCTTAT 1113
Qy 912 GATCTGGCTTCTCCAAAATGAGATGCCAAGAGATACATCAGGCAACTCCACACAT 971
Db 1114 CTCATTAACAGAGATGCCAAGCATGAGCAAGAACTATATTCACCTTTGATCAGATG 1173
Qy 972 CCTGCGCCAGATTAGCAGAAAGTTTCCCTCATGTGAAACCATTGGCTATTGATGTC 1031
Db 1174 CCGAAGATGAACCTTGGCAATGTATTTATGTCGCAATCCCTGGCTGTGACTGGCTG 1233
Qy 1032 GATAAATGTGACATTCGATCTACTAGAAATTTACAGTTGAGAGACATTAGATCAT 1091
Db 1234 GAGAAGATGCTTGTATGTGACTCAGATTAAGAATTTACAGGCGCCCAAGCCCTTGACAT 1293
Qy 1092 CCCTTACCTTGCAGAAAGCTCCAGATGACAGTGAACACC 1129
Db 1294 GCTTACTTGTCTCAGTACACGATCCTGATGATGAACC 1331

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RESULT 13
US-08-605-002A-11
Sequence 11, Application US/08605002A
Patent No. 5871934

GENERAL INFORMATION:
APPLICANT: Lee, John C.
APPLICANT: Adams, Jerry L.
APPLICANT: Gallagher, Timothy F.
APPLICANT: Green, David W.
APPLICANT: Livi, George P.
APPLICANT: McDonnell, Peter
APPLICANT: McNulty, Megan M.
APPLICANT: McNulty, Dean E.
APPLICANT: Strickler, James E.
TITLE OF INVENTION: Drug Binding Protein
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation

```

: STREET: Corporate Intellectual Property/P.O. Box
: STREET: 1539
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0939
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/605,002A
: FILING DATE: 15-APR-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Hecht, Elizabeth J.
: REGISTRATION NUMBER: P-41,824
: REFERENCE/DOCKET NUMBER: P-41,824
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 270-5009
: TELEFAX: (610) 270-5090
: INFORMATION FOR SEQ ID NO: 11:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3813 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: CELL TYPE: Monocyte
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 379..1461
:
: US-08-605-002A-11
:
: Query Match 13.4%; Score 232; DB 2; Length 3813;
: Best Local Similarity 56.5%; Pred. No. 2.2e-54;
: Matches 496; Conservative 0; Mismatches 370; Indels 12; Gaps 3;

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GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 19, 2003, 22:59:26 ; Search time 63 Seconds

(without alignments)
793.158 Million cell updates/sec

Title: US-09-623-034-2

Perfect score: 1987

Sequence: 1 MADANMGAGGGGPPDFPSVL.....EEQIKDMITQELSLNPEYA 375

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	18	AAW15512
2	1764.5	88.8	423	18	AAW15513
3	1523	76.6	398	22	AAAB48048
4	1500	75.5	398	22	AAAB48047
5	1498.5	75.4	395	21	AAAG31653
6	1493	75.1	374	22	AAAB48046
7	1490	75.0	374	21	AAAG34157
8	1488.5	74.9	382	21	AAAG31654
9	1487.5	74.9	366	21	AAAG31655
10	1482	74.6	393	19	AAW61252

11	1365	68.7	330	21	AAAG34158
12	1349.5	67.9	372	21	AAAG33123
13	1349.5	67.9	372	22	AAAB48044
14	1344.5	67.7	376	21	AAAG04672
15	1334	67.1	358	21	AAAG31124
16	1309	65.9	371	21	AAAG45420
17	1290	64.9	316	21	AAAG34159
18	1244.5	62.6	373	21	AAAG30672
19	1219	61.3	372	21	AAAG42613
20	1219	61.3	406	21	AAAG42612
21	1217	61.2	372	21	AAAG06702
22	1217	61.2	379	21	AAAG06701
23	1204.5	60.6	354	21	AAAG30978
24	1134	57.1	311	23	AAAG5837
25	1117	56.2	367	21	AAAG44793
26	1117	56.2	368	21	AAAG35746
27	1117	56.2	368	21	AAAG44792
28	1117	56.2	370	21	AAAG35745
29	1117	56.2	370	21	AAAG44791
30	1117	56.2	370	22	AAAB48045
31	1117	56.2	434	21	AAAG35744
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33	1087	54.7	367	21	AAAG44680
34	1087	54.7	369	21	AAAG44679
35	1086	54.7	369	22	AAAB48043
36	1078	54.3	370	21	AAAG31572
37	1073	54.0	370	21	AAAG77976
38	1069	53.8	376	21	AAAG53018
39	1067.5	53.7	350	21	AAAG31573
40	1061	53.4	366	21	AAAG29650
41	1061	53.4	368	21	AAAG29649
42	1061	53.4	422	21	AAAG29648
43	1058.5	53.3	356	21	AAAG3019
44	1048	52.7	280	21	AAAG04673
45	1048	52.7	338	21	AAAG31574

ALIGNMENTS

RESULT 1	
ID	AAW15512
AAW15512	standard; protein: 375 AA.
AC	AAW15512;
DT	04-JUN-1997 (first entry)
DE	MAP kinase #1.
KW	MAP kinase #1.
KW	Mitogen activated protein kinase; MAP; infectious specific protein;
KW	plant; jasmonic acid.
OS	Synthetic.
PN	JP09065881-A.
PD	11-MAR-1997.
XX	11-MAR-1997.
PF	29-AUG-1995; 95JP-0220935.
XX	29-AUG-1995; 95JP-0220935.
PR	29-AUG-1995; 95JP-0220935.
XX	(NORQ) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
PA	WPI: 1997-220416/20.
XX	N-PSDB; AAT60349.
DR	Wound-stress inducible MAP kinase - used to regulate the synthesis
PT	of jasmonic acid
XX	Claim 2; Page 13-14; 21pp; Japanese.

CC AAM1512 and AAM1513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues 201-203. The MAP kinase and its gene can be used
 CC to regulate the synthesis of jasmonic acid and the synthesis of a group
 CC of infectious specific proteins. By introducing the MAP kinase gene into
 CC a plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonic acid and a group of infectious
 CC specific proteins can be regulated in the plant.

XX Sequence 375 AA;

Query Match 100.0%; Score 1987; DB 18; Length 375;
 Best Local Similarity 100.0%; Pred. No. 4.7e-198;

Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADANMAGGQPPDPSPVLTGGQYVQDFGNEFFETTKYRPPIMPICGAGYICSV 60
 DB 1 MADANMAGGQPPDPSPVLTGGQYVQDFGNEFFETTKYRPPIMPICGAGYICSV 60
 QY 61 LNFELNEMVAVKKIYANAFDIYMDAKRTLRKILRHLDHENVIGLRDVIPLRREFSDV 120
 DB 61 LNFELNEMVAVKKIYANAFDIYMDAKRTLRKILRHLDHENVIGLRDVIPLRREFSDV 120
 QY 121 YIATELMDTDLHQIIRSNQIGSEDCQYFMYQLRGKLYHSANVLRDLKPSMLYAN 180
 DB 121 YIATELMDTDLHQIIRSNQIGSEDCQYFMYQLRGKLYHSANVLRDLKPSMLYAN 180
 QY 181 CDLKICFGLARPNIEENMTEYVTRMYRAPPELLNSTDYTAIDWVSCITMELN 240
 DB 181 CDLKICFGLARPNIEENMTEYVTRMYRAPPELLNSTDYTAIDWVSCITMELN 240
 QY 241 KPLFGKDHVHQIRLTELGTPTLADLGLQNEADAKRYIRQLPQHPROQLAEVPHVNP 300
 DB 241 KPLFGKDHVHQIRLTELGTPTLADLGLQNEADAKRYIRQLPQHPROQLAEVPHVNP 300
 QY 301 LAIDLVRKMLTFDPTTRKITYEALDHPYLAKLHDAGDEPTCPVPSFDFEQQIGIEBOIK 360
 DB 301 LAIDLVRKMLTFDPTTRKITYEALDHPYLAKLHDAGDEPTCPVPSFDFEQQIGIEBOIK 360
 QY 361 DMIVQEALSLNPEYA 375
 DB 361 DMIVQEALSLNPEYA 375

RESULT 2
 AAM1513

ID AAM1513 standard; protein; 423 AA.

XX AAM1513;

AC 04-JUN-1997 (first entry)

XX MAP kinase #2.

DE Mitogen activated protein kinase; MAP; infectious specific protein;

XX Plant; jasmonic acid.

XX Synthetic.

XX JP09065881-A.

XX 11-MAR-1997.

XX 29-AUG-1995; 95JP-0220935.

XX 29-AUG-1995; 95JP-0220935.

XX (NORO) NORINSUISANSNO NOGYO SEIBUTSU SHIGEN.

XX WPI; 1997-220416/20.

XX DR N-PADB; AAT60350.

XX

PT Wound-stress inducible MAP kinase - used to regulate the synthesis
 PT of jasmonic acid
 XX
 PS Claim 3; Page 16-17; 21pp; Japanese.

CC AAM1512 and AAM1513 represent the mitogen activated protein (MAP)
 CC kinases of the invention. This sequence contains the T-E-Y sequence, in
 CC which the threonine and tyrosine residues are phosphorylated to activate
 CC the protein at residues 249-251. The MAP kinase and its gene can be used
 CC to regulate the synthesis of jasmonic acid and the synthesis of a group
 CC of infectious specific proteins. By introducing the MAP kinase gene into
 CC a plant, thereby inducing expression of the mRNA for MAP kinase (or its
 CC antisense RNA), the synthesis of jasmonic acid and a group of infectious
 CC specific proteins can be regulated in the plant.

XX Sequence 423 AA;

Query Match 88.8%; Score 1764.5; DB 18; Length 423;
 Best Local Similarity 97.7%; Pred. No. 8.3e-175;

Matches 336; Conservative 1; Mismatches 4; Indels 3; Gaps 1;

QY 32 FGNFEITTKYRPPIMPICGAGYICSVLTTELNEMVAVKKIYANAFDIYMDAKRTLRK 91
 DB 83 FGNFEITTKYRPPIMPICGAGYICSVLTTELNEMVAVKKIYANAFDIYMDAKRTLRK 91
 QY 92 KLRHLDHENVIGLRDVIPLRREFSDVYIATELMDTDLHQIIRSNQIGSEDCQYFM 151
 DB 143 KLRHLDHENVIGLRDVIPLRREFSDVYIATELMDTDLHQIIRSNQIGSEDCQYFM 151
 QY 152 QLRGLKLYHSANVLRDLKPSMLYANCDLKICDFGLARPNIEENMTEYVTRMYRA 211
 DB 200 QLRGLKLYHSANVLRDLKPSMLYANCDLKICDFGLARPNIEENMTEYVTRMYRA 211
 QY 212 PELLNSTDYTAIDWVSCITMELNRRKPLFGKDHVHQIRLTELGTPTLADLGL 271
 DB 260 PELLNSTDYTAIDWVSCITMELNRRKPLFGKDHVHQIRLTELGTPTLADLGL 319
 QY 272 QNEADAKRYIRQLPQHPROQLAEVPHVNPPLAIDLVDKMLTFDPTTRKITYEALDHPYLAK 331
 DB 320 QNEADAKRYIRQLPQHPROQLAEVPHVNPPLAIDLVDKMLTFDPTTRKITYEALDHPYLAK 379
 QY 332 LHDAGDEPTCPVPSFDFEQQIGIEBOIKDMIVQEALSLNPEYA 375
 DB 380 LHDAGDEPTCPVPSFDFEQQIGIEBOIKDMIVQEALSLNPEYA 423

RESULT 3
 AAB48048

ID AAB48048 standard; protein; 398 AA.

XX AAB48048;

XX 19-MAR-2001 (first entry)

XX Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;

XX auxin; cytokinin; gibberellin; immunogen.

XX Zea mays.

XX WO200070059-A2.

XX 23-NOV-2000.

XX 28-APR-2000; 2000WO-US11687.

XX 14-MAY-1999; 99US-0134292.

XX 08-JUL-1999; 99US-0142996.

XX (PION-) PIONEER HI-BRED INT INC.

XX Helentjaris TG;

XX

XX WPI: 2001-031929/04.
DR N-PSDB: AAC84265.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX Claim 13; Page 97; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.
XX
XX Sequence 398 AA;
SQ
Query Match 76.6%; Score 1523; DB 22; Length 398;
Best Local Similarity 72.9%; Pred. No. 1.1e-149;
Matches 283; Conservative 44; Mismatches 45; Indels 16; Gaps 3;
QY 1 MADANMAGGCGGFDPF-----SVLHGGGYOYOFDFGNFFETTKYRPP1 46
DB 12 MTDAGLG-GGGOPPPPOQPPAGSGAMENIHATLSHGCRFIOYNIFGVNFEVTSKXKPP1 70
QY 47 MPIGRGAYGIVCSVLTENLNMVAVKKTANAFDIYMDAKRFLREIKLRHLDHENYIGLR 106
DB 71 LPIGKAGVIGVCSALNSETAEVAKITANAFDNKIDAKRFLREIKLRHMDHENYIVAIR 130
QY 107 DVIPPLLRERSDYIAELMDTDJHOITIRSNQGLSEBHCYFMQGLRGKYTHSANVL 166
DB 131 DIIPPLLEARNDYIAELMDTDJHOITIRSNQGLSEBHCYFLYQILRGKYTHSANVL 190
QY 167 HRDLKPSNLLVANCNDLKCDFGLARPIENENMTEYVTVRYRAPPELLNSSDXTAID 226
DB 191 HRDLKPSNLLNANDLKCDFGLARTSETDFMEYVTVRYRAPPELLNSSSETTAID 250
QY 227 VWSVGCIFMELMNRKPLFGKDHVHQIRLLTELLGTPTEADLGLQNEADAKRYIQOLPOH 286
DB 251 VWSVGCIFMELMNRKPLFGKDHVHQIRLLTELLGTPTEADLGLQNEADAKRYIQOLPOH 309
QY 287 PROQLAEVFPVNPPLAIDLVMKLTEDPTRRITVEALDHYRLAKLHAGDEPICIPOVPS 346
DB 310 ARQSEPFKEFPHVOPLAIDLVEKMLTEFPRQRTVEGALHAPYLASLHIDSEPVCSMPFS 369
QY 347 FDFEEOGIGEBQIKDMIVQEALSLNPEY 374
DB 370 FDFEEOHALSEQMKDLIVQEALAFNPDY 397
RESULT 4
AAB48047
ID AAB48047 standard; protein: 398 AA.
XX
AC AAB48047;
XX
DT 19-MAR-2001 (first entry)
XX
DE Signal transduction protein.

XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
KM auxin; cytokinin; gibberellin; immunogen.
XX
XX Zea mays.
XX WO200070059-A2.
XX
XX 23-NOV-2000.
XX
XX 28-APR-2000; 2000WO-US11687.
XX
XX 14-MAY-1999; 99US-0134292.
PR 08-JUL-1999; 99US-0142996.
XX
XX (PION-) PIONEER HI-BRED INT INC.
PA
PI Helentjaris TG;
XX
XX WPI: 2001-031929/04.
DR N-PSDB: AAC84262.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX Claim 13; Page 94; 126pp; English.
XX
XX The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.
XX
XX Sequence 398 AA;
SQ
Query Match 75.5%; Score 1500; DB 22; Length 398;
Best Local Similarity 71.9%; Pred. No. 2.7e-147;
Matches 279; Conservative 45; Mismatches 48; Indels 16; Gaps 3;
QY 1 MADANMAGGCGGFDPF-----SVLHGGGYOYOFDFGNFFETTKYRPP1 46
DB 12 MSEAGAG-GGGOPPPQPLRPVGGGYMLDNICATLSHGCRFIOYNIFGVNFEVTSKXKPPV 70
QY 47 MPIGRGAYGIVCSVLTENLNMVAVKKTANAFDIYMDAKRFLREIKLRHLDHENYIGLR 106
DB 71 LPIGKAGVIGVCSALNSETAEVAKITANAFDNKIDAKRFLREIKLRHMDHENYIVAIR 130
QY 107 DVIPPLLRERSDYIAELMDTDJHOITIRSNQGLSEBHCYFMQGLRGKYTHSANVL 166
DB 131 GIIPPAQRAAFNDYIAELMDTDJHOITIRSNQGLSEBHCYFLYQILRGKYTHSANVL 190
QY 167 HRDLKPSNLLVANCNDLKCDFGLARPIENENMTEYVTVRYRAPPELLNSSDXTAID 226
DB 191 HRDLKPSNLLNANDLKCDFGLARTSETDFMEYVTVRYRAPPELLNSSSETTAID 250
QY 227 VWSVGCIFMELMNRKPLFGKDHVHQIRLLTELLGTPTEADLGLQNEADAKRYIQOLPOH 286
DB 251 VWSVGCIFMELMNRKPLFGKDHVHQIRLLTELLGTPTEADLGLQNEADAKRYIQOLPOH 309

QY 287 PROOLAEVFFHVNPLAIDLVDMKMTFDPTRITVEALDHPYLAKHDAGDEPTICPVFFS 346
Db 310 PROSLPEKFPVHVOPLAIDLVEKMLTFDPORITVEGALHPHYLASHDISDEPCSMFFS 369
QY 347 FDFEOGIGGEIOIKDMITVOEALSLNPEX 374
Db 370 FDFEOHALSEOMKDLITVOEALNPNPDY 397
RESULT 5
AAG31653
ID AAG31653 standard; Protein: 395 AA.
XX
AC AAG31653;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38048.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 07-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134258.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
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PR 01-JUN-1999; 99US-0137222.
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PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
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PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142803.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
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PR 23-JUL-1999; 99US-0145218.
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PR 27-JUL-1999; 99US-0145818.
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PR 28-JUL-1999; 99US-0145951.
PR 28-JUL-1999; 99US-0146386.
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PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.

CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.
XX
SQ Sequence 374 AA;
Query Match 75.18; Score 1493; DB 22; Length 374;
Best Local Similarity 72.08; Pred. No. 1.3e-146;
Matches 265; Conservative 59; Mismatches 44; Indels 0; Gaps 0;
QY 7 GAGGQPPDPFSPVLTGHGQVQDFDIFGNFEITKYPRIIMPICRGAYGVICSVLTNELN 66
Db 5 GVDGAPVAEFGQYTHGGRFLQYNIFFGNLEITKQYOPMPICRGAYGVICSVNSETK 64
QY 67 EMVAVKKIAPAFDIYMDAKRTLRREIKLRHLDHENVIGLRDVPPLRREFSDYIATEL 126
Db 65 EMVAIKKIAPAFDNDHMDAKRTLRREIKLRHLDHENIIGIRVYIPRPVQAFNDYIGTEL 124
QY 127 MDTDLHOIIRSNGLSEDCOYFWOLRGLKYTHSANVLRHDIKPSNLVANCCLKIC 186
Db 125 MDTDLHHIIRSNGLSEHSQYFWYQILRGLKYTHSANVLRHDIKPSNLVANCCLKIC 184
QY 187 DFGIARINIEENMTVEYVFWYRAPPELLNSSDYTAIDVWVGCIEMELNKKPLFCG 246
Db 185 DFGIARPSSESDMTVEYVFWYRAPPELLNSTDYSAIDWVGCIEMELNKKPLFCG 244
QY 247 KDHVHOIRLTLLGTPTEDLGLQNEADAKRYIROLPOHRRQOLAIEYFPHVPLAIDL 306
Db 245 RDHMQRLTEVIGTPTDELGFIRNBDAAKRYRHLRQFRRRFVSLFPRMQVALDLI 304
QY 307 DKMTLPTPRTIYEEALDHYLAKLDAGDEPTCPVPFSDFEQGIGEEQIDMTIYQE 366
Db 305 ERMILTFPRLQIYEEALEHRYLRHLDVADPCTDFPSDFRQOALTEDOMKQLIFE 364
QY 367 ALSINPEY 374
Db 365 AMELNPNF 372
RESULT 7
AAG34157
ID AAG34157 standard; Protein; 374 AA.
XX
AC AAG34157;
XX
DT 18-OCF-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 41518.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.
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PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
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PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
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PR 18-JUN-1999; 99US-0139461.
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PR 28-JUN-1999; 99US-0140823.
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PR 01-JUL-1999; 99US-0141842.
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PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.

KW termination sequence.
XX Arabidopsis thaliana.
XX EPI033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123518.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.
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PR 22-JUL-1999; 99US-0145089.
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PR 23-JUL-1999; 99US-0145145.
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PR 02-AUG-1999; 99US-0146386.
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Query Match 74.9%; Score 1488.5; DB 21; Length 382;
Best Local Similarity 72.3%; Pred. No. 4e-146;
Matches 272; Conservative 49; Mismatches 42; Indels 13; Gaps 2;

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RESULT 9
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ID AAG31655 standard; Protein; 366 AA.
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AC AAG31655;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38050.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 29-OCT-1999; 990S-0162142.

Query Match 74.9%; Score 1487.5; DB 21; Length 366;
Best Local Similarity 74.7%; Pred. No. 4.8e-146;
Matches 269; Conservative 49; Mismatches 41; Indels 1; Gaps 1;

QY 15 DFPVLTGCGOYVQDFGFFELTTKRRPMPDYGATGYCSVLTENKAVAKKI 74
DB 6 NIPATLSHGGRFTQYNIFGNIFEWTAKYKPPIMPIGAGYICSAANSETNESVAIKKI 65
QY 75 ANAFDIYMDAKRTLREIKLRLHDEHENVIGLRVYIPPLRRESVDYIATELMDTDLHOI 134
DB 66 ANAFDNKIDAKRTLREIKLRLHDEHENVIAIROIIPPLRNANVDYIATELMDTDLHOI 125

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QY 135 IRSNGLSEDHCOYFMYOLLRLGLKTYHSANVLRDLKPSNLLVNNANCDLKICDFGLARN 194
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Db 126 IRSNALSEHCOYFLYOLILRLGLKTYHSANVLRDLKPSNLLNANCDLKICDFGLART 185
QY 195 IENENMTEYVTRWYRABELLNNSDYTAIDVMSVGCIFMELMNRKPLFGSKDHVHQR 254
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 SESDFMTEYVTRWYRABELLNNSDYTAIDVMSVGCIFMELMDRKPLFGSDHVGHR 245
QY 255 LTELIGPTEADLGFONEDAKRYIRQLPQHPROQLAEVPHVNPPLAIDLVKMLTDP 314
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Db 246 LLMELIGPSEEELEFL-NEAKRYIRQLPQHPROQSTIDKPEPTVPHLIDLEKMLTDP 304
QY 315 TRRTIVEBALHPYLAKLHDAGDEPICVPFSFDEFOQIGEEQIKDMTYOALSLNPEY 374
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Db 305 RRRIVLDAALAHPLYLNSLHDISDEPECTIPFNFDFENHALSEQMKELIYREALAFNPEY 364

RESULT 10
AAM61252 standard; Protein: 393 AA.
XX AC AAM61252;
XX DT 22-SEP-1998 (first entry)
XX DE Salicylic acid induced MAP kinase.
XX KW Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
XX KM tobacco; disease resistance; microbial pathogen; MAP kinase.
XX OS Nicotiana sp.
XX PN W09818939-A1.
XX PD 07-MAY-1998.
XX PE 24-OCT-1997; 97WO-0519219.
XX PR 21-APR-1997; 97US-0837593.
XX PR 25-OCT-1996; 96US-0029805.
XX PA (RUTE ) UNIV RUTGERS STATE NEW JERSEY.
XX PI Klessig DF, Zhang S;
XX DR WPI: 1998-272230/24.
XX DR N-PSDB: AAV27563.
XX PT Salicylic acid induced MAP kinase - obtained from tobacco, used to
XX PT produce plants having increased disease resistance, against e.g.
XX PT microbial pathogens
XX PS Claim 28; Pages 62-63; 97pp; English.
XX CC This represents a salicylic acid induced protein (SIP) kinase. This SIP
XX CC kinase is an unique member of the mitogen-activated protein (MAP) kinase
XX CC family. The salicylic acid induced MAP kinase of the invention comprises
XX CC kinase subdomains I to XI of serine/threonine kinases. The protein is
XX CC activated by an agent that induces a disease defence response in plants
XX CC by way of a signal transduction pathway that is at least partially
XX CC dependent on salicylic acid. Host plant cells transformed with a vector
XX CC containing a recombinant DNA molecule encoding the salicylic acid induced
XX CC MAP kinase is used to produce the protein recombinantly. The products can
XX CC be used to produce plants with increased disease resistance. The products
XX CC may also be used as a research tool to identify other proteins involved
XX CC in the hypersensitive response and systemic acquired response in plants.
XX Sequence 393 AA;
Query Match 74.6%; Score 1482; DB 19; Length 393;
Best Local Similarity 71.5%; Pred. NO. 2e-145;
Matches 274; Conservative 46; Mismatches 51; Indels 12; Gaps 2;
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Db 9 DTMMDAGAGOPPTAPQVYAGMDNIPATLSHGGRFLQINPFENITEVATAKAPPLIPICK 68
QY 52 GAYGIVCSVLTNLENMVAVKRIANAFDIYMDAKRTLREIKLRLDHENVGLADVIRP 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 69 GAYGIVCSALNSETIENVAIKRIANAFDIAKRTLREIKLRLDHENVGLADVIRP 128
QY 112 PLRREFSDVYIATLEMDTDLHOIIRSNGLSEDHCOYFMYOLLRLGLKTYHSANVLRDLK 171
    | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Db 129 POREAFNPNVYIAYLEIMDDDLHOIIRSNGLSEHCOYFLYOLILRLGLKTYHSANVLRDLK 188
QY 172 PSNLLVNNANCDLKICDFGLARTSETDFTMTEYVTRWYRABELLNNSDYTAIDVMSVG 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 189 PSNLLNANCDLKICDFGLARTSETDFTMTEYVTRWYRABELLNNSDYTAIDVMSVG 248
QY 232 CIFMELMNRKPLFGSKDHVHQRIRLTLELGTPTLEADLGFONEDAKRYIRQLPQHPROQL 291
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Db 368 HALTEQMKELIYRESLAFNPEY 390

RESULT 11
AAG34158 standard; Protein: 330 AA.
XX ID AAG34158
XX AC AAG34158;
XX DT 18-OCT-2000 (first entry)
XX DE Zea mays protein fragment SEQ ID NO: 41519.
XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX KW termination sequence; corn.
XX OS Zea mays subsp. mays.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PE 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
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XX PR 25-MAR-1999; 99US-0126264.
XX PR 29-MAR-1999; 99US-0126785.
XX PR 01-APR-1999; 99US-0127462.
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67.9%; Score 1349.5; DB 21; Length 372;

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QY 63 TELNEMVAVKKIAPFDIYMDAKTLEIKLRHLDHENVYGLDVPPLPAREFSVYI 122
Db 59 SQSGEEVAIKKVGNAFNNHIDAKRTLEIKLRHMDHENILALDVIAPPRENFNDVYI 118
QY 123 ATELMDDTLHOIIRNSOGLSEDCQYFMYOLLRLGKTYIHSANVLRDLKPSNLLVANNCD 182
Db 119 VTELMDDTLHOIYRSNOPLTDHCQYFLYOLRLRLKTYIHSANVLRDLKPSNLLVANNCD 178
QY 183 LKICDFGLARPNIENMTEYVTRWYRAPPELLNSSDYTAIDVWSGCIEMELMNKP 242
Db 179 LKIDFGIARFTSETDTEYVTRWYRAPPELLNCSQYTAIDVWSGCIETAVTRP 238
QY 243 LFGKRDVHQIRLTTELTGTEADLGTIONEDAKRYTRQLPQHPROQLAEVFPVNP 302
Db 239 LFGKRDVHQIRLTTELTGTEADLGTIONEDAKRYTRQLPQHPROQLAEVFPVNP 302
QY 303 IDLVKMLTEPDRTRITVEALDHPYLAKLHDADDEPICVPFSEDOGIGEOIKDM 362
Db 299 VDLLERLMVFDPSSRRIYVDEALHHPYLAHLEINDEPFCRAPFSEDOGIGEOIKEL 358
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Db 359 IWRSLAFNPE 369
RESULT 13
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AC AAB48044;
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DT 19-MAR-2001 (first entry)
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DE Signal transduction protein.
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KW zea mays; maize; signal transduction protein; phytohormone; ethylene;
auxin; cytokinin; gibberellin; immunogen.
XX

OS Zea mays.
XX
XX WO200070059-A2.
XX
XX 23-NOV-2000.
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XX 28-APR-2000; 2000WO-US11687.
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XX 14-MAY-1999; 98US-0134292.
XX 08-JUL-1999; 99US-0142996.
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XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Helentjaris TG;
XX
XX WPI: 2001-031929/04.
XX N-PSDB: AAC84253.
XX
XX New signal transduction nucleic acids and encoded proteins useful for
PT regulating phytohormone expression, including ethylene, auxins,
PT cytokinins and gibberellin, to provide control of plant response to
PT environmental stresses -
XX
XX
XX Claim 13; Page 85-86; 126pp; English.

CC The invention provides Zea mays signal transduction proteins and encoding
CC nucleotide sequences. The nucleic acids are useful for regulating
CC expression of phytohormones, including ethylene, auxins, cytokinins,
CC and gibberellin, to effect developmental changes in plants and provide
CC control of plant response to environmental stresses. They may also be
CC used as probes or amplification primers in the detection, quantitation or
CC isolation of gene transcripts, for detecting mutations in the gene, for
CC monitoring upregulation of expression or changes in enzyme activity in
CC screening assays of compounds, for detection of any number of allelic
CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
CC further be used for recombinant expression of their encoded polypeptides,
CC as immunogens in the preparation or screening of antibodies, and in sense
CC or antisense suppression of genes in a host cell, tissue or plant. The
CC proteins may be used in assays for enzyme agonists or antagonists, as
CC immunogens or antigens to obtain antibodies specifically immunoreactive
CC with the proteins. The present sequence represents a signal transduction
CC protein of the invention.

XX Sequence 372 AA:

Query Match 67.9%; Score 1349.5; DB 22; Length 372;

Best Local Similarity 64.7%; Freq. No. 1,1e-131;

Matches 240; Conservative 66; Mismatches 62; Indels 3; Gaps 1;

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DB 59 SOSGEVAIAIKKYGNAFDNHIDAKRTLRKILRHMDHENIILAKDYIRPRENNNDYVI 118
QY 123 ATELMDTDLHQIRSNQGLSEHCQYFMVQLLRGLKYIHSANVLRDLKPSMLNANCD 182
DB 119 VTELMDTDLHQIRSNQPLTDHCOYFLYQLLRGLKYVSAHILHRDLKPSMLFNANCD 178
QY 183 LKICDFGLARPIENENNTTEYVTRMYRAPPELLNSSDYTAIDWASVGCIMELMNRCP 242
DB 179 LKIDFGIARTSETDMLTEYVTRMYRAPPELLNCSQYTAIDWASVGCILGEIVTRQP 238
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DB 299 VDLERMLVFPDSRRITVDEALHPYLASLHEINDEPTCPAPFSDFPQSTFEAHIKEL 358

QY 363 IYQEALSLNPE 373
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160771.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 67.7%; Score 1344.5; DB 21; Length 376;
Best Local Similarity 65.3%; Pred. No. 3.9e-131;
Matches 243; Conservative 63; Mismatches 65; Indels 1; Gaps 1;

QY 2 ADANMAGGGGFPDPSPVLHGGQYVQFDIFGNFETTTKYRPPIMPICGAGIVCSVL 61
Db 3 AESCFGSSGDO-SSSKGVATFHGSGSYOVYVYGNLFVSRKRVPLRPIGKAGYIVCAAR 61
QY 62 NTELNENVAVKKINAKADIWDARKRLRETKLRLHLDHENYIGLRDVIIPPLRREFSDYV 121
Db 62 NSERGEVIAIKIGNARDNIIIDARKRLRETKLRLKHMDEHNVIAVKDIIPQRENFDYV 121

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:53:56 ; Search time 4374 Seconds

(without alignments)
11477.444 Million cell updates/sec

Title: US-09-623-034-1

Perfect score: 1725

Sequence: 1 tatatacacatatctca.....gagcaagagactgtgata 1725

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pin:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

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39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1725	100.0	1725	6	E12716	E12716 Tobacco CDN
2	1725	100.0	1725	6	TOBWIPIK	D61317 Tobacco mRN
3	1320	76.5	1786	6	E12717	E12717 Tobacco CDN
4	1127.2	65.3	1644	8	AF247135	AF247135 Capsicum
5	738.4	42.8	1495	8	AF149424	AF149424 Ipomoea b
6	716	41.5	1695	8	MSMK4	X82270 M.sativa MM
7	713.8	41.4	1643	8	AF153061	AF153061 Pisum sat
8	684	39.7	1480	8	AF386961	AF386961 Arabidops
9	684	39.7	1309	8	AY090981	AY090981 Arabidops
10	682.4	39.6	1370	8	ATHTATMPK3	D21839 Arabidops
11	677.2	39.3	1565	8	PCMAPKINA	Y12785 Petroselinu
12	577.2	33.5	1597	8	NTP45NMF4	X83880 N.tabacum m
13	574.4	33.3	1485	8	AB062138	AB062138 Solanum t
14	566.2	32.8	1617	8	AB062139	AB062139 Solanum t
15	561.6	32.6	1458	8	AF247136	AF247136 Capsicum
16	559.4	32.4	1423	8	AF242308	AF242308 Euphorbia
17	552	32.0	1544	6	AR084240	AR084240 Sequence
18	552	32.0	1544	6	NTP94192	U94192 Nicotiana t
19	548.4	31.8	1529	8	ALFERKMAP	L07042 Medicago sa
20	545.2	31.6	1512	8	MSMSK7	X66469 M.sativa MR
21	543.6	31.5	1522	8	PSMAP	X70703 P.sativum m
22	534	31.0	1197	6	AX048758	AX048758 Sequence
23	533.4	30.9	1197	6	AX048762	AX048762 Sequence
24	532.2	30.9	1562	8	ATHTATMPK6	D21842 Arabidops
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27	494	28.6	1125	6	AX048754	AX048754 Sequence
28	488.2	28.3	1452	8	AF079318	AF079318 Trifolium
29	485	28.1	1520	8	ASMAP1	X79993 A.sativa As
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32	483.2	28.0	1356	8	OSA486975	AJ46975 Oryza sat
33	483.2	28.0	1396	8	AF216315	AF216315 Oryza sat
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35	483	28.0	1551	8	AB055515	AB055515 Nicotiana
36	481.8	27.9	1754	8	NTP43NMF6	X83879 N.tabacum m
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45	458.6	26.6	1529	8	AB062140	AB062140 Solanum t

ALIGNMENTS

RESULT 1

LOCUS E12716 1725 bp DNA linear PAT 27-APR-1998

DEFINITION Tobacco cDNA encoding a wound induced protein kinase.

ACCESSION E12716

VERSION E12716.1 GI:3251548

KEYWORDS JP 1997065881-A/1.

SOURCE Nicotiana tabacum.

ORGANISM Nicotiana tabacum

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Solanales: Solanaceae: Nicotiana.

REFERENCE Ohashi, Y. and Seo, S.

AUTHORS 1 (bases 1 to 1725)

TITLE WOUND STRESS INDUCING MAP KINASE AND ITS GENE

JOURNAL
 Patent: JP 1997065881-A 1 11-MAR-1997;
 NORIN SUISANSYO NOGO SEIBUTSU SHIGEN KENKYUSHO
 COMMENT
 OS Nicotiana tabacum
 PN JP 1997065881-A/1
 PD 11-MAR-1997
 PF 29-AUG-1995 JP 1995220935
 PI OHASHI YUKO, SEO SHIGEMI
 PC C12N15/09,C07K14/415,C12N5/10,C12N9/12,C12P7/40,C12P7/42, PC
 C12P7/62,
 PC C12P19/44,C12P21/02, (C12P7/40,C12R1:91), (C12P7/42,C12R1:91),
 PC (C12P7/62,
 PC C12R1:91), (C12P19/44,C12R1:91), (C12P21/02,C12R1:91); CC
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 CC topology: Linear;
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 FT /clone_idb='CDNA from tobacco leaves 2 days
 FT after infection
 FT With tobacco mosaic virus in lambda ZAP11 FT
 FT vector
 FT /clone='DS22'
 FT 114..1241
 FT /product='wound induced protein kinase' FT
 FT /gene='WIPK'.
 FT /organism='Nicotiana tabacum'
 FT /db_xref='Caxon:4097'
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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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 Db 1 TATATATACACAAATGCTCATATTTACACTTATTTACATGATCTGTCTTAAT 60
 Oy 61 TAGGCACATATTTTTCTTTCTTGAGCTAATTAAGACGTAATTAATCATGGCTG 120
 Db 61 TAGGCACATATTTTTCTTTCTTGAGCTAATTAAGACGTAATTAATCATGGCTG 120
 Oy 121 ATGCAAAATATGGGTGCGCGGTGAGGCAATTCCTCATTTCTCGGTGTTAACTCAG 180
 Db 121 ATGCAAAATATGGGTGCGCGGTGAGGCAATTCCTCATTTCTCGGTGTTAACTCAG 180
 Oy 181 GCGGACATATGTACAGTTTGATATTTTGGTAATTTCTTTGAGATCACTACCAAGTATC 240
 Db 181 GCGGACAAATGTATACAGTTTGATATTTTGGTAATTTCTTTGAGATCACTACCAAGTATC 240
 Oy 241 GTCCTCTATTTATGCGTATTTGGTCGGGCGCTTATGAGATTCGTCCTCGGTGTAATA 300
 Db 241 GTCCTCTATTTATGCGTATTTGGTCGGGCGCTTATGAGATTCGTCCTCGGTGTAATA 300
 Oy 301 CGGAGCTGATGAGATGGTTCAGATTAGAAAAATCGCGAATCGGTTGATATTTACATGG 360
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 Db 361 ATGCTAAGAGGAGCTCTCCGTGAGATTAACTCTCCGCGCATTTAGACCGAAAAAGTAA 420
 Oy 421 TTGGTTTAAAGACGATGATCTCCACACCTTACGAAGGAGATTTCTGATGTTTACATGG 480
 Db 421 TTGGTTTAAAGACGATGATCTCCACACCTTACGAAGGAGATTTCTGATGTTTACATGG 480
 Oy 481 CTACTGAATCAATGATGATCTTCCACCAATAATTGATCCAAACCAAGGTTTATCAG 540

[illegible]

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Db 1681 TTGCTTCGTATGATTTATCCAAACAAGACAAGACTGTGTGATA 1725
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RESULT 2
TOBWIPK 1725 bp mRNA linear PLN 12-FEB-1999
LOCUS Tobacco mRNA for WIPK, complete cds.
DEFINITION D61377
ACCESSION D61377.1 GI:1136297
VERSION D61377.1 GI:1136297
KEYWORDS WIPK.
SOURCE Nicotiana tabacum cDNA to mRNA, clone WIPK.
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; eunasterids I; Solanales; Solanaceae; Nicotiana.
1 (sites)
REFERENCE Seo,S., Okamoto,M., Seto,H., Ishizuka,K., Sano,H. and Ohashi,Y.
Tobacco MAP kinase: a possible mediator in wound signal
transduction pathways
JOURNAL Science 270 (5244), 1988-1992 (1995)
MEDLINE 96123271
REFERENCE 2 (bases 1 to 1725)
AUTHORS Ohashi,Y.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1725)
AUTHORS Ohashi,Y.
TITLE Direct Submission
JOURNAL Submitted (26-JUN-1995) Yoko Ohashi, National Institute of
Agricultural Resources, Department of Molecular Biology;
Kannonnai 2-1-2, Tsukuba, Ibaraki, Japan
(E-mail:yohashi@res.abr.affrc.go.jp., Tel:0298-38-7440,
Fax:0298-38-7408)
FEATURES
Location/Qualifiers
source 1..1725
/organism="Nicotiana tabacum"
/db_xref="taxon:4097"
114..1241
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BASE COUNT 469 a 361 c 326 g 569 t
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Query Match 100.0%; Score 1725; DB 8; Length 1725;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

LOCUS E12717 1786 bp DNA linear PAT 27-APR-1998
 DEFINITION Tobacco cDNA encoding a wound induced protein kinase.
 ACCESSION E12717.1 GI:3251549
 VERSION JP 1997065881-A/2.
 KEYWORDS Nicotiana tabacum.
 SOURCE Nicotiana tabacum
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; eunasterids I; Solanales; Solanaceae; Nicotiana.
 1 (bases 1 to 1786).
 Ohashi, Y. and Seo, S.
 WOUND STRESS INDUCING MAP KINASE AND ITS GENE
 Patent: JP 1997065881-A 2 11-MAR-1997;
 NORIN SUIJANSYO NOGYO SEIBUTSU SHIGEN KENKYUSHO
 OS Nicotiana tabacum
 PN JP 1997065881-A/2
 PD 11-MAR-1997
 PE 29-AUG-1995 JP 1995220935
 PI OHASHI YUKO, SEO SHIGEMI
 PC C12N15/09, C07K14/415, C12N5/10, C12N9/12, C12P7/40, C12P7/42, PC C12P7/62,
 PC C12P19/44, C12P21/02, (C12P7/40, C12R1:91), (C12P7/42, C12R1:91),
 PC (C12P7/62,
 PC C12R1:91), (C12P19/44, C12R1:91), (C12P21/02, C12R1:91); CC
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 CC topology: Linear;
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 FT /cultivar="Samsun NN
 FT /clone_lib="cDNA from tobacco leaves 2 days
 FT after infection
 FT with tobacco mosaic virus in lambda ZAPIT FT
 FT vector'

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 Matches 1342; Conservative 0; Mismatches 5; Indels 9; Gaps 1;
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 DB 971 ACCGAGCTTTTGTAACTCTTCAGATTTACACTGCTGCTATAGATGTTGTTGTTGCTG 1030
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 DB 1031 TTGATCTTATGGAATCTTATGAATAGAAAACCTTTTGTGTTGGAAGAAATCATGTACA 1090
 QY 866 TCAAAATGCGTTGTTAACCGGCTTTTGGACCCCAAGAAAGCTGATGTGGCTTCCT 925
 DB 1091 TCAAAATGCGTTGTTAACCGGCTTTTGGACCCCAAGAAAGCTGATGTGGCTTCCT 1150
 QY 926 CCAAAATGAAGATGCAAAAGATATCATCAGGCAACTCCCAACATCTCCGCGAGAGTT 985
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 QY 986 AGCAGAAATTTTCCCTCATGTGAACCCATTTGCTATTGATCTTGTGATTAATTTTGAC 1045
 DB 1211 AGCAGAAATTTTCCCTCATGTGAACCCATTTGCTATTGATCTTGTGATTAATTTTGAC 1270
 QY 1046 ATTGATCTTACTAGAAAGATTTACAGTTGAGAAAGCATTTGATCATCACTGACCTGAAA 1105
 DB 1271 ATTGATCTTACTAGAAAGATTTACAGTTGAGAAAGCATTTGATCATCACTGACCTGAAA 1330

QY 1106 GCTCCAGATGACGAGTACCAACGATGCGCCGTGTCATTCTCCTTTGACTTGAGA 1165
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Db 1331 GCTCCACGATGACAGGTGACGACCAACGATCTGCCCTGTCATTCTCTTTGACTTGAGA 1390
QY 1166 ACAAGGAATAGGAGAAGACCAATTAAGACATGATATATCAGAACTTTGCTCACTGAA 1225
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Db 1391 ACAAGGAATAGGAGAAGACCAATTAAGACATGATATATCAGAACTTTGCTCACTGAA 1450
QY 1226 TCCTCAATATGCTTAACATAAGACAATCTCTCTTCCTGCTTCCCTTTGATC 1285
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Db 1451 TCCTCAATATGCTTAACATAAGACAATCTCTCTTCCTGCTTCCCTTTGATC 1510
QY 1286 TGGAGATCTACTCTCTCTGCTGATTTCTTGGCGAGCAGGACATCAATGTTTT 1345
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QY 1346 GCTCACTGCTAGTCCCTTGGCAACTGTATGTAAGCAGCCTTCAATGTGACCCAT 1405
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Db 1571 GCTCACTGCTAGTCCCTTGGCAACTGTATGTAAGCAGCCTTCAATGTGACCCAT 1630
QY 1406 CTATATATCTTTTATTTTATTTTATTTATGAGTGTCTGTGAGCTAGCTTTGGGCA 1465
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Db 1631 CTATATATCTTTTATTTTATTTTATTTATGAGTGTCTGTGAGCTAGCTTTGGGCA 1690
QY 1466 CTTGATATTTCTATGATATTTGCTACCTCCGCGACAGACAACATTAATATCTCCAC 1525
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Db 1691 CTTGATATTTCTATGATATTTGCTACCTCCGCGACAGACAACATTAATATCTCCAC 1750
QY 1526 TCATTTCTATGATTTGATCTGTGTGTGATTTCA 1561
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Db 1751 TCATTTCTATGATTTGATCTGTGTGTGATTTCA 1786

RESULT 4
AF247135 1644 bp DNA linear PLN 03-JUL-2000

LOCUS AF247135 1644 bp DNA linear PLN 03-JUL-2000
DEFINITION Capsicum annuum MAP kinase 1 (MK1) gene, complete cds.
ACCESSION AF247135
VERSION AF247135.1 GI:8925320
KEYWORDS

SOURCE Capsicum annuum.
ORGANISM Capsicum annuum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; euasterids I; Solanales; Solanaceae; Capsicum.
REFERENCE 1 (bases 1 to 1644)
Back,K., Han,O., Shin,H.-U. and Kim,K.-U.
Molecular cloning and cultivar specific expression of MAP kinase
from Capsicum annuum
Unpublished
JOURNAL 2. (bases 1 to 1644)
REFERENCE Back,K. and Shin,D.-H.
AUTHORS Direct Submission
TITLE Submitted (18-MAR-2000) Genetic Engineering, Chonnam National
JOURNAL University, 300 Youngdong-Dong, Kwangju 500-757, South Korea
FEATURES
source
1. 1644
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cds
124..1251
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HSANVTHDLKPSNILLANLNDLKTCDGLRAPLENEMTEYVTRNRAPELLNS
SDYEALIDWASVGCETEMELNMRKPLFPAKDHVHOLRLTELGLPTESDLSFLRNEDA
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BASE COUNT 452 a 329 c 328 g 535 t
ORIGIN

Query Match 65.3%; Score 1127.2; DB 8; Length 1644;
Best Local Similarity 84.9%; Pred. No. 1.2e-254;
Matches 1332; Conservative 0; Mismatches 203; Indels 33; Gaps 5;

QY 1 TATATATACATATGCTATATTTACACTTATTCATGTTCATATGATCTGTCTAT 60
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QY 61 TAGGCACATATTTTTTCTTTCTTGAGCTAGATTAAGGACAGAAATTAATTCATGGCTG 120
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Db 131 ATGCAATATGGGTGGCGGTGAGTCAATTCCTGATTTCTCTCAACATGTGACTACAG 190
QY 181 GGGGACAAATATGATACGATTTGATATTTTGGTAATTTCTTGATAGACTACCAAGTATC 240
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QY 241 GTCTCTCTATATAGCTATATGCTGCTGCTTATGGAATTTCTGCTGCTGCTGGAATA 300
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Db 251 GGCCTCTCTATATAGCTATATGCTGCTGCTTATGGAATTTCTGCTGCTGCTGGAATA 310
QY 301 CGGAGCTGAATAGATGGTTCAGTTAAGAAAATGCGCAATGCGTTTATTTACATGCG 360
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Db 311 CGGAGCTGAATAGATGGTTCAGTTAAGAAAATGCGCAATGCGTTTATTTACATGCG 370
QY 361 ATGCTAAGAGAGCTCCGCTGAGATTAAGCTCCGCTGCTTAAAGCAATGGAATATGTA 420
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Db 371 ATGCTAAGAGAGAGCTCCGCTGAGATTAAGCTCCGCTGCTTAAAGCAATGGAATATGTA 430
QY 421 TTGGTTTAAAGAGAGTATCTCCACCCCTTACGAAGGAGTTTCTGATGTTTACATG 480
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Db 491 CTACGAACTCATGATATGATATCTTACCAAAATATTTAGATCCAAACCAAGTTATCG 550
QY 541 AGGATCAGCTGAGTACCTCATGATATGATATCTTCCGCTGAGCTTAAATATCATATTCG 600
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Db 551 AGGATCAGCTGAGTACCTCATGATATGATATCTTCCGCTGAGCTTAAATATCATATTCG 610
QY 601 CGAATGTTCTTCATAGAGATCTCAAAACGAGCAACCTTTTGGTAAATGCAAAATGTGATC 660
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Db 611 CGAATGTTCTTCATAGAGATCTCAAAACGAGCAACCTTTTGGTAAATGCAAAATGTGATC 670
QY 661 TTAAGATATGATCTTGGTCTTGTAGGCGCAAAATAGAGACGAGATATAGCGAAT 720
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Db 671 TTAAGATATGATCTTGGTCTTGTAGGCGCAAAATAGAGACGAGATATAGCGAAT 730
QY 721 ATGTTGTAAACGAGATGTCAGAGGACAGAGCTTTTGTGAACCTTCAGATTCAGT 780
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Db 731 ATGTTGTAAACGAGATGTCAGAGGACAGAGCTTTTGTGAACCTTCAGATTCAGT 790
QY 781 CTGCTATAGATTTTGTGCTGCTGCTGATCTTCAATGGAACCTTATGAAATGCAAACTT 840
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Db 791 AAGCCATAGACCTTTGTGCTGCTGATCTTCAATGGAACCTTATGAAATGCAAACTT 850
QY 841 TGTTTGGGAAAGATCATGATACAAATAGCGTTGTAACGAGGCTTGTGGACCC 900
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Db 851 TGTTTGGGAAAGATCATGATACAAATAGCGTTGTAACGAGGCTTGTGGACCC 910

QY	876	TTGTTAAACCCGAGCTTCTTGCGACACCCCAACAGAGCTGATCTTGCGTTCTCTCCAAATGAA	935
Db	822	TTAAATACCCGAGCTTCTTGCGACACCAACCGATTCCTCGATCTTAATGAGATGA	881
QY	936	GATGCAAGAGATACATAGCGCAATCCACAACTCCTCGGCACAGTATACAGAAATG	995
Db	882	AATGCAAAAGGTATATATAGCGCAACTTTCACACTACGTCCACGCCAGCAGTTAGCAAAATGCT	941
QY	996	TTCCCTCATGTGAACCCATTGGCTATTGATCTTGTGCATAAATGTTGCATTCGATCCT	1055
Db	942	TTCCACACAGTGCATCCTTTAGCCATTGATCTCATGATGAATAAATGTTGCATTTAAACCC	1001
QY	1056	ACTAGAGAATTTACAGTTGAGGAGACANTAGATCATCTCCCTACCTTGCAAAAGCTCCACGAT	1115
Db	1002	TCCAAAATAATTTACAGTTGAGGAGAACCATTAGTCTATCCCTCACTTGCCTGACCATGATGAC	1061
QY	1116	GCAGGTGACGAACCATCTGCGCTGTTCACATCTCTTGACTTGAGCAACAAAGGAATA	1175
Db	1062	AAATCTGATGAACCCCATATGCCCGGTTCCATTAC---TGATTTGAGAAACAAACCTAT	1118
QY	1176	GGAGAGAGCAAAATTAAGACATGATATATACAGAAAGCTTGTCACTGATCACTGAATAT	1235
Db	1119	GGAGAGAGCAAAATTAAGACATGATATTAACGAGGAGCACTGGCAATGATACAGAGATAT	1178
QY	1236	GCTTAACATTAAGAGAAATCAATTTCTTCTCTCTGTTTCCCT	1279
Db	1179	GCATTAACAAGAGGCGACTACCATTTTCTCCCTTTCTTCTCCCT	1222

RESULT 6			
LOCUS	MSMK4		
DEFINITION	MSMK4	1695 bp	linear
ACCESSION	X82270		
VERSION	X82270.1		
KEYWORDS	MMK4 gene; protein kinase.		
SOURCE	Medicago sativa.		
ORGANISM	Medicago sativa		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.		
REFERENCE	1 (bases 1 to 1695)		
AUTHORS	Jonak,C.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-OCT-1994) C. Jonak, Inst Microbiol. & Genetics, Vienna Biocenter, Dr. Bohr Gasse 9, 1030 Wien, AUSTRIA		
REFERENCE	2 (bases 1 to 1695)		
AUTHORS	Jonak,C., Kiegerl,S., Ligterink,W., Barker,P.J., Huskisson,N.S. and Hilt,H.		
TITLE	Stress signaling in plants: a mitogen-activated protein kinase pathway is activated by cold and drought		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 93 (20), 11274-11279 (1996)		
MEDLINE	97008170		
PUBMED	8853346		
FEATURES			
source	Location/Qualifiers		
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gene			
CDS			

BASE COUNT		490		a	317	c	345	g	543	t	
ORIGIN											
Query Match		41.5%: Score 716; DB 8; Length 1695;									
Best Local Similarity		78.5%: Pred. No. 7e-158;									
Matches 857; Conservative		0; Mismatches 235; Indels 0; Gaps 0;									
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Db	200	TGCGGATTTTCGGGGTTCAATCAGCGGCGACATTTGGTATACAAACGTTGCG	259								
OY	211	GTAATTTCTTGGATCACAAGTATCGTCTCTATTATGCTTATTTGGTGTG	270								
Db	260	GTAATCTTTGAGGTTACGGGGAAGTATCGCTCCCATCATGCCGATTTGGTGTG	319								
OY	271	CTTATGGAATGTGCGCGGTTGGATPACGGACCTGAAGATGGATGGTACAGTTA	330								
Db	320	CTTACGGAATGTTGTTGCTGTTGGTAAATACGGAACAAATGATGGTTGCTGTGA	379								
OY	331	AAATGCGCAATGCGTTTGATATTTACATGATGCTAAAGAGCACTCCGTGAGATT	390								
Db	380	AGATGCGCAATGCTTTTGATATCATATGATGCGCAACGTAACGCTAGGTGATT	439								
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Db	440	TTCTTAGGCATTTAGATCATGAAATGTAATTTGGTTTAAGATTTTATCTCCAC	499								
OY	451	TACGAAGGAGTTTCTGATGTTTCATTTGCTACTGACACTATGATATGATCTT	510								
Db	500	TGCGTAGAGAGTTTATATGATGCTACATACACCAGCAACTCATGATCTTCA	559								
OY	511	AAATATATGATCCAACCAAGGTTTATCAGAGGATCACTGTCAGTTCATGTAT	570								
Db	560	AGATTTATTCGCTCCATCAAAATCTCTGTGATGAACATGCGCAGTATTTTGT	619								
OY	571	TGCCCGGCGCCTAAATACATACATTCGCGGAATGCTTCATGTAGATATGCA	630								
Db	620	TTCTTCGTTGGGTTAAGTATATACATTCGCAAAATATATCATAGAATTTGA	679								
OY	631	GCAACCTTTGGTAAATCCAAATGTTGATCTTAAATATGTAATTTGGTCTG	690								
Db	680	GCAACCTGTTGTTGATGCAAAATTCGCACTTGAATATTTGTTGGTGTG	739								
OY	691	CAACATAGAGACAGAGATATGACGGAATATGTTGTAAACAGATGTACAGG	750								
Db	740	CAACATAGAGAAATGACTTTCATGACAGATATGTTGTCAAAAGATGATAG	799								
OY	751	AGCTTTGTTGAACCTTTCAGATTACACTGCTGCTATATGATTTGGTCTG	810								
Db	800	AATTTATTTGTGAACCTTCAGATTACACTCTGCAATATGATGTCTGTTG	859								
OY	811	TCTTATGGAACCTTTGATAGAAAACCTTTGTTGGGAAAAATATGATG	870								
Db	860	TTTTTATGAGCTTATGATATAAAAGCCCTGTTTCCGTGGCAAGATATG	919								
OY	871	TACGCTTTTAACGAGCTTCTGGCACCCCAACAGAAAGTATCTTGGCTT	930								
Db	920	TGCGCTTTATGACAGGCTTCTTGGCACTCAACATGACGCTGATGTGG	979								
OY	931	ATGAAGATGCAAGAGATACATCAGGCAATCCCAACATCTCCGACAGTA	990								
Db	980	ATGACGATGCGGAAGATATATCCGCAAACTTCCATATCTCTGAACCTT	1039								
OY	991	AAGTTTCCCTCATGTGAACCATGGCTATTGATCTTGTGATAAATGTTG	1050								
Db	1040	GGGTTTTCCTCCATGTATCTCCCTTAGGCATTTGTTGATATAATGTTG	1099								
OY	1051	ATCTACTAGAAGATTACAGTTGAGAGCAATTAGATCATCCTTGCAAG	1110								
Db	1100	ATCTCAGCAAGAAATTCAGTTGAAGAGCACTGGCCATCATCTTCAAAA	1159								

QY	1111	ACGATGACGAGGAGACACCGATCCCGCTGTTCCATTCCTCCCTGACCTTACGTAACAAACAG	1170
DB	1160	ATGATGATGCCGATACACCTATCTGACATGACACCACTTCTCATTGATGATTGACAAACAGC	1219
QY	1171	GAAATGAGGAAGACCAATTAAGACATGATATATACAGAAAGCTTTGTCACGTGATCCTG	1230
DB	1220	ATTGTGATGAGAACCAATTAAGAGATGATATACAGGAGGACGATTAACACTCATCATCTG	1279
QY	1231	AATATGCTTAA	1242
DB	1280	AGTATGCTTAA	1291
RESULT 7			
LOCUS	AF153061	1643 bp	mRNA
DEFINITION	Plum sativum MAP kinase 3 (mapk3)	linear	PLN 11-DEC-2000
ACCESSION	AF153061		complete cds.
VERSION	AF153061.1	GI:8132286	
KEYWORDS			
SOURCE	Plum sativum.		
ORGANISM	Plum sativum.		
REFERENCE	1 (bases 1 to 1643)		
AUTHORS	Marcote, M.J. and Carbonell, J.		
TITLE	Transient expression of a pea MAP kinase gene induced by gibberellic acid and 6-benzyladenine in unpollinated pea ovaries		
JOURNAL	Plant Mol. Biol.	44 (2), 177-186	(2000)
PUBMED	21003323		
REFERENCE	11117261		
AUTHORS	2 (bases 1 to 1643)		
TITLE	Marcote, M.J. and Carbonell, J.		
JOURNAL	Submitted (21-MAY-1999)		
FEATURES	Location/Qualifiers		
source	1. 1643		
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BASE COUNT	501 a 304 c 327 g 511 t		
ORIGIN			
Query Match	41.4%	Score 713.8;	DB 8; Length 1643;
Best Local Similarity	78.3%;	Pred. No. 2.3e-157;	
Matches	856; Conservative	0; Mismatches 237; Indels	0; Gaps 0;
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DB	89	TGCGGAGTCCCGCGGCTTGACACTCAACGGTGGACAGTTCCTCAATACACAGCTTTTCG	148
QY	211	GTAATTTCTTGAGATCACTACCAAGATATGCTCTCTATTAATGCTATTTGCTGCTG	270

Db	149	GTATCTCTTTGAGAGTTACTGCTGCTAAGTATGCTGCTCCATCATGCGCATTTGGTCGGCGC	208
Oy	271	CTTATGGAATTTGCTGCTCGGTGTTAAATACGAGCTGATGAGATGGTTGCAGTTAAGA	330
Db	209	CTTACGGAATCGTTTGTTCCTCTTGAACACGAGACGAAATGATGGTTCTGCTGTAGA	268
Oy	331	AAATCGGAATGGGTTTGATATTACATGATGAGTGAAGGAGCTGCTCGGTGAGTTAAG	390
Db	269	AAATAGCGAATGCTTTTCGATATATCAATGATGATGCCAAGCGTACGCTGCGTGAATTAAAC	328
Oy	391	TCCTCGGCATTTAGACCATGAAATGATATTGGTTTAAAGACGCTGATTCCTCACCT	450
Db	329	TTCTTAGGCAATTAGATCATGAAATAGTCATTTGGTTTAAAGATGTTATTCCTCACCT	388
Oy	451	TACGAAGGAGTTTTCGATGTTTACATTTGCTACGTAATCATGATGGATATCTTCAAC	510
Db	389	TGCGTTAGAGGTTTAAATGATGCTCATATACCAACCGAATCCATGATCTTCAATC	448
Oy	511	AAATAAATTAATCCACACCAAGGTTTATCGAGAGTACGTCGATCTTCAATGATAGC	570
Db	449	AAATCATTCGCTCCAAATCAAAATCTGTCAGATGTAACACGTCGTACTTTTGTATGAGA	508
Oy	571	TCCTCGGCTGCTAAATATACATCAATTCGCGGAGTTCCTCATGAGATCTCAACCGA	630
Db	509	TTCTCTGCTGAGACGAGGTATATATCATCTTGCACCAACTTATCATGAGATTTGAAGCCA	568
Oy	631	GCAACCTTTGGTGTAAATGCACAAATTTGATCTTAAATATGATGACTTTGCTGTGCTAGC	690
Db	569	GCAATCTGTTGCTGAAATGACAAATTTGGGACTTGAAGATTTATTTTGGTCTTGGCGGC	628
Oy	691	CAAAACATAGAGAACGAGATATGACGGAATATGTTGTAAACGATGTTACAGGCAACCAG	750
Db	629	CAACTATGAGAAATGACTTCATACAGAAATATGATGATCAAGATGATAGAGCTCTCG	688
Oy	751	AGCTTTGGTGAAGCTCTTGATTAACAGCTGCTAATAATGTTGGTGGCTGCGGTTGCA	810
Db	689	AATTTGTTGTAAGTCTCTGATTTACAACCTCTGCCATGATGTTTGGTCTGTTGGTTGTA	748
Oy	811	TCCTTCATGAGAACTTATGATAATGAAGAAACCTTTGTTGGTGAAGAAAGATCATGTACATCAA	870
Db	749	TCCTTCATGAGAGCTTATGATAATGAAGAAACCTTATTTCTGGCAAGACCATGATGATGAGA	808
Oy	871	TACGCTTGTTAACCGAGCTTCTTGGACCCCAACGAAGCTGATGTTGGGCTTCCCTCCAAA	930
Db	809	TGCGCTTATGACAGAGCTTCTTGGACATCCCACTGACCTGATGTCGGTTAGTGAAGAA	868
Oy	931	ATGAAAGATGCAAGAGATATACATGAGGCACTCCACAAACATCCTGCGCAGCAGTTAGCAG	990
Db	869	ATGAAGATGCAAGAAAGATATATCCGCAACACTTCCTCAATATCTCGCCACCTTAAATA	928
Oy	991	AAAGTTTCCCTCATGTGACCCCATTTGGCTATTTGATCTTGCATAAATGTTGACATTCG	1050
Db	929	GGGTTTTCCTCCCATGTTCAATCCCTTGGCCATCGATCTCATCATGATAAATGTTGACAATTG	988
Oy	1051	ATTCCTACGAAAGATTAACGTTGAGAGAAGCATTTAGATATGCTTACCTTGCAGAAAGCTCC	1110
Db	989	ATCCCATCTAGAAAGATACAGTGGTGAAGAAAGACATGACCATCTCATACCTTGAAAAACATC	1048
Db	1049	ACGATGTAGCTGATGAAGCCCATCTGCATGAGAACATTTCTCATTTGATTTGAACAAAGC	1108
Oy	1171	GAAATAGGAAGAAAGCAAAATTAAGGACATGATATATACGAGAACCTTTGTCATGAAATCCTG	1230
Db	1109	ATTGTAAGCAAGAGCAAAATTAAGAGATGATCTACAGGAGGACATTTACACTCAATCCTG	1168
Oy	1231	AATATGCTTAAAC 1243	
Db	1169	AGTACGCTTAAAC 1181	

AF386961	1480 bp	mRNA	linear	PLN 14-JUN-2001
LOCUS				
DEFINITION	Arbidiopsis thaliana mitogen-activated protein kinase 3 (F9K21.220)			
ACCESSION	AF386961			
VERSION	AF386961			
KEYWORDS	complete cds.			
ORGANISM	Arbidiopsis thaliana.			
SOURCE	Arbidiopsis thaliana.			
REFERENCE	Arbidiopsis thaliana.			
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 1480)			
	Lam, B., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Cheuk, R., Chung, M. K., Hayashizaki, Y., Ishida, J., Kamiya, J., Kawai, J., Kim, C., Lin, J., Liu, S. X., Narusaka, M., pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R. W.			
TITLE	Direct Submission			
JOURNAL	Submitted (30-MAY-2001) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA			
COMMENT	e-mail for correspondence: arab@sequence.stanford.edu			
	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.			
	The Salk, Stanford, PGSC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Lam, B., Karlin-Neumann, G., Nguyen, M., Southwick, A., Miranda, M., Palm, C. J., Bowser, L., Jones, T., Banh, J., Chen, H., Cheuk, R., Chung, M. K., Kim, C., Lin, J., Liu, S. X., Pham, P. K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.			
	Lam, B., (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R. W. (SSP/Stanford) contributed equally to this work as pIs.			
FEATURES	Location/Qualifiers			
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DEFINITION	Arabidopsis thaliana mRNA for MAP kinase, complete cds.		PLN 05-FEB-1999

KEYWORDS MAP kinase; mitogen activated protein kinase; serine/threonine kinase.

SOURCE Arabidopsis thaliana (strain:Columbia) CDNA to mRNA.

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 1370)

AUTHORS Mizoguchi, T., Hayashida, N., Yamaguchi-Shinozaki, K., Kamada, H. and Shinozaki, K.
TITLE ATPPKs: a gene family of plant MAP kinases in *Arabidopsis thaliana*
JOURNAL FEBS Lett. 336 (3), 440-444 (1993)

REFERENCE 2 (bases 1 to 1370)
AUTHORS Shinozaki, K.
TITLE Direct Submission
JOURNAL Submitted (29-OCT-1993) kazuo Shinozaki, Tsukuba Life Science

COMMENT
Kazuo Shinozaki
Submitted (29-Oct-1993) to DBJ by:
Tsukuba, the Inst. of Physical and Chemical Res., 3-1-1 Kohyada,
Tsukuba, Ibaraki 350, Japan (E-mail: shinozaki@tcsa.riken.go.jp,
Tel.:0298-36-4359, Fax:0298-36-9060)
Submitted (29-Oct-1993) to DBJ by:

The Institute of Physical and
Chemical Research (RIKEN)
3-1-1 Koyakakai, Tsukuba
Ibaraki 305
Japan
Phone: 0298-36-4359
Fax: 0298-36-0060
Location/Organizers

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 1 (bases 1 to 1565)
 Ligierink,W., Kroj,T., zur Nieden,U., Hirt,H. and Scheel,D.
 Receptor-mediated activation of a MAP kinase in pathogen defense of
 plants
 JOURNAL Science 276 (5321), 2054-2057 (1997)
 MEDLINE 97342856
 PUBMED 9197271
 REFERENCE 2 (bases 1 to 1565)
 AUTHORS Kroj,T.
 TITLE Direct Submission
 JOURNAL Submitted (25-APR-1997) T. Kroj, Institut fuer Pflanzenbiochemie,
 Stress- und Entwicklungsbiologie, Weinberg 3, D-06120 Halle,
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 1 (bases 1 to 1597)
 Wilson, C., Anglimayer, R., Vicente, O. and Heberle-Bors, E.
 Molecular cloning, functional expression in Escherichia coli, and
 characterization of multiple mitogen-activated-protein kinases from
 tobacco
 Eur. J. Biochem. 233 (1), 249-257 (1995)
 MEDLINE 96061956
 PUBMED 7588752
 REFERENCE 2 (bases 1 to 1597)
 AUTHORS Wilson, C.
 TITLE Direct Submission
 JOURNAL Submitted (13-JAN-1995) C. Wilson, Institute for Microbiology and
 Genetics, Vienna Biocenter, University of Vienna, Dr. Bohr Gasse 9,
 A- 1030 Vienna, AUSTRIA
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 OY 1169 AGAATTAGAGAGAGAGAGAGATTTAAGACATGATATATGAGAGAGCTTTGCTACGATTC 1228
 Db 1322 TGCCCTTACTGAGAGAGAGAGAGAGATTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1381
 OY 1229 TGAATA 1234
 Db 1382 TGAATA 1387
 RESULT 13
 AB062138 1485 bp mRNA linear PLN 24-MAY-2002
 LOCUS Solanum tuberosum StmPr1 mRNA for mitogen-activated protein kinase,
 DEFINITION complete cds.
 ACCESSION AB062138
 VERSION AB062138.1 GI:21165522
 KEYWORDS

CDS	119..1303	/gene="StmK2"	/codon_start=1	/product="mitogen-activated protein kinase"	/protein_id="BA893530.1"	/db_xref="GI:21165525"	/translation="MDGSAQOQDTVMGSDAAGQOPATPPLPMAGMENIPATLSHGRRF IQVYFNGINEFVATKRYKPPIMPIGKAGYGVCSALNSETNEHVAIKRIANAFDKRIDAK KRTLRTEIKLIRHMDHENIVAIRDIIPPORAEFNDYIAVELMPTDQILIRSGSLSS EHCQYQYLOILRMDKRTIHSANVLRKIDPKNLLNLCQKICDFGLARTSETDM TEYVTRFMYRPPELLNNSDYTAIDVWSYGCIMELMDRPLFPGSDHYQLTLMEL LIGPSAEEMFELNENAKRTIROLPIYLRQSFVKFPHVNPALIDYVKMTLFPKRR LVGGAALHPILTSLHDIDSEPCMPFSPDFEQHALTEQMKELIYREGIALTFNPETQ HM"
BASE COUNT	458 a	311 c	332 g	516 t			
ORIGIN							
Query Match	32.8%	Score 566.2;	DB: 8;	Length 1617;			
Best Local Similarity	71.1%	Pred. NO. 1.2e-122;					
Matches 764; Conservative	0;	Mismatches 308;	Indels 3;	Gaps 1;			

OY	160	TTCCGCGTTTAACTACGCGGACCAATATAGTACACTTTGATATATTTTGGTATTTCT	219
Db	219	TTCCGCGCACCGTGTGAGTACGGGTGGCGGGTTTATTCATACAACTTTTGGTATATAT	278
OY	220	TTGAGATGACTACCAAGATATCGTCCCTCATTTATTCCTATTGCGTGTGTATGGAA	279
Db	279	TTGAAGTTACTGSCAAGAATATAAGCCTCCCAATTATGCCAATCGGTAAAGAGCTTATGGTA	338
OY	280	TTTGTCTGCTCGGTGTTGAATAACGAGCTGAATGAGATGGTTGACGTTAAGAAAATGCGCA	339
Db	339	TTGTTGTCTGCTTCTTGGATTCGGAGCAAAATGAACATGTTGCATTAAGAAAATTTGCCGA	398
OY	340	ATGCGTTTGATATTACATGATGCTATAGAGAGCTCTCCGAGATTAAGCTCCCTCCGCC	399
Db	399	ATGCTTTTGATPACAAAATTTGATGCGCAAGAGAACTTTCCTGTGAGATCAAGCTTCTTGAC	458
OY	400	ATTTAGACCATGAAAATTTAAATTGGTTTAAAGAGACGATTCCTCCACCCTTACGAAAGG	459
Db	459	ATATGATGATGAAAATATTGTTGGATTAAGATATATATTCACACCTCAAGAGAAAG	518
OY	460	AGTTTTCGATGTTTACATTGCTACTGAATCATGATACGTATCTTCAACCAATATTA	519
Db	519	CATTAAATGATGTCATATTGCTATGAGCTTATGAGACATGATCTCCATCAAAATTAATTC	578
OY	520	GATCCAACCAAGGTTTATCAGAGATTCACGTCACTACTTCAATGATATAGCTCCCTCGTG	579
Db	579	GCTCTTAATCAAGGATTATCAGAGAACATTTGCCAATATTTCTTGATATAGATCCCTCGTG	638
OY	580	GCCCTAAATPACATACATTCCGCGAATGTTCTTCATPAGAGATCTCAACCGAGACACCTTT	639
Db	639	GGTTGAATPACATACATTCTCGAAATGTTTTCGATAGGAGACTTGAAGCTTACCAATCTCC	698
OY	640	TGTTAAATGCAAAATTTGTGATCTTAAAGATATGTGACTTTGGCTTTCAGGCCAAACATAG	699
Db	699	TCTTAATGCCAATTTGATTTAAAGATATATGATTTTGGGCTTCTGCTGTACACTCTCG	758
OY	700	AGAACGAAATATGACGGAATATGTTGTAAACAGATGTAAGGCGACACAGACTTTGT	759
Db	759	AAACGACTTTATGACCCAAATATGTTGTGACAAAGATGTAACCGACCTCCGAGCTGTGT	818
OY	760	TGAATCTTCGAGTATACACTGCTGCTATAGATGTTTGGTCTCGGTGTCACATCTTCATGG	819
Db	819	TAAATTTCTTGACTATACTGACGCTATATGATGCTGTGCTCAATTTGTCATTTTCATGG	878
OY	820	AACTATTAAATGAAAACCTTTGTTGGTGAAGAAAGATCATGTACATAAATACCTTGT	879
Db	879	AACTGATGGACGAAGAAGCTCTGTTTCTCGTGAAGATCATGTAAACGACGTACGTCGCG	938
OY	880	TAAACGAGCTTCGGAACCCACAGAAAGCTGATCTTGCTTCTCCAAAATGAAGATG	939
Db	939	TTATGAGCTTGATGGACCCCTTCTTGAGGCGGAATGGAGTTT---GAATGGAATG	995

OY	940	CAAAAGATACATCAGGCAACTCCCAACACATCTCCGCCAGCAGTTAGCAGAGTTTTC	999
Db	996	CAAAACGGGTACATCATGACAACTTCCTCTTTACCGCGCAATTCATTGTTAAAAATTTC	1055
OY	1000	CTCATGTACACCCATATGGCTATTGATCTCTTGTCGATAAATGTGACATTCGACTCTACTA	1059
Db	1056	CACATGTAAACCCCTGCTCTCTATTGATCTCTGTGGAAAAATGTGACATTGATCCCAAA	1115
OY	1060	GAGCATTTACAGTTGAGAGAACATTAGATCATTCCTTACCTTGCAAAAGCTCCACGATGCAG	1119
Db	1116	GGAGCTTACGTGTGTAAGGCGCGCTTGACACACCTTACCTAAACGCGTTATGATATTA	1175
OY	1120	GTGAGAACCCATCCTGCCCTGTCCATCTCTCTTGACTTTGAGCAACAAAGAATAGAG	1179
Db	1176	GTGAGACGCCGTTTGCATGACTCCTTTTACCTTGATTTTGAACAGATGCGCCTTACCG	1235
OY	1180	AAGACCAATTBAGSACATGATATATTCAGAAAGCTTTGTCACTGATCTTGATA	1234
Db	1236	AGGAACCAATTAAAGACGCTGATTTTACAGGAGGAGCTTTGACATTTATCCCAATA	1290

RESULT	15
AF247136	1458 bp DNA linear PLN 03-JUL-2000
LOCUS	
DEFINITION	Capsicum annuum MAP kinase 2 (MK2) gene, complete cds.
ACCESSION	AF247136
VERSION	AF247136.1 GI:8925322
KEYWORDS	
SOURCE	
ORGANISM	Capsicum annuum. Capsicum annuum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Asterales; euasterids I; Solanales; Solanaceae; Capsicum. 1 (bases 1 to 1458) Back,K., Han,O., Shin,H.-Y. and Kim,K.-U. Molecular cloning and cultivar specific expression of MAP kinase from Capsicum annuum Unpublished 2 (bases 1 to 1458) Back,K. and Shin,D.-H. Direct Submission Submitted (18-MAR-2000) Genetic Engineering, Chonnam National University, 300 Youngbon-Dong, Kwangju 500-757, South Korea
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
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BASE COUNT	393 a 284 c 321 g 460 t
ORIGIN	
Query Match	32.6%; Score 561.6; DB 8; Length 1458;
Best Local Similarity	70.6%; Pred. NO. 1.5e-121;
Matches 763; Conservative	0; Mismatched 314; Indels 3; Gaps 1;

Search completed: May 19, 2003, 22:21:28
Job time : 4383 secs

OY	155	TGTTTTTCCTGGTTTTAACTACGCGGACAAATATGACAGTTTGGATTTTGGTAA	214
Db	96	TAAACATTCACGCCACGTTTGATGACCGGTGGCCGGTTATTCAATATATACATATTTGGTAA	155
OY	215	TTTCTTTCAGATCTACTACCAAGATATGCTCTCTCTATATATGCTTAATTTGGTGGTGTCTTA	274
Db	156	TGTAATTTGAAGTTATCTGCACAAAGTATAAGCCCTCAATTAATGGCAATTTGGTAAGGAGCTTA	215
OY	275	TGGAAATGTCTGCTCGGTGTTGAATACGAGCTGAATGAGATGTTTGGCAGTTAAGAAAT	334
Db	216	TGGCATTTGTGTTCTCTCTTTGAATTCGGAGACGAATGAGACATGTTGGCACAAAGAAAT	275
OY	335	CGCAGATGCGTTTGATATTTACATGATGCTAGAGAGCTTCGCCGAGATTAAGCTCT	394
Db	276	TGGCAATGCTTTTGATTAACAAATTAATGATGCAAGAAAGAGTTGCGTGAATACAACTCT	335
OY	395	CCGCCATTTAGACCATGAAAAATGTAATGTTTAAAGACGTGATTTCTCCACCCTTACG	454
Db	336	TGCGACATATGGATCATATAAATATGTTGGGATCAGAGACATATATTCACCTCCCTCAAG	395
OY	455	AAGGAGATTTCTGATGTTTACATGGTACTAGCACTGATGACATGATGATGATCACTCAAT	514
Db	396	GGAAGCATTTATGATGTTCTATATTTGCATATGAGCTTATGAGACATGATCTTCATCAAT	455
OY	515	AATTAGATCCAACCAAGTTTATCAGAGATCCGATCTACTGATCTCATGATATCACTCT	574
Db	456	TATTGCTCTATATCAGGAGTTATCAGAGAACTTTGCTAGTATTTCTTGTATCAATCT	515
OY	575	CCGTTGGCTAAATACATACATATCCGGAATGTTCTTCAATAGAGATCTCAACCGAGCA	634
Db	516	CCGTGGGTTGAATTAACATACATATCTGCAATGTTTGGCATAGGAGATTTGAACCTTAGAA	575
OY	635	CCTTTGGTAAATCAATATTTGATCTATAGATATGATCTTGGCTTGTAGAGCCAAA	694
Db	576	TCTCTCTTGAATGCAAAATTTGATTTAAAGATATGTATTTTGGGTACAGCTCGTGTAC	635
OY	695	CATGAGACGACAAATTTGACGGAAATTTGTTTAAACAGATGTRACAGGACACAGACT	754
Db	636	TTTGGAAACCTCACTTTATGACCGAGATATGTTGGACAAAGATGATGTCAGCTCCGAGACT	695
OY	755	TTTTTGAACCTTCACATATTAACCTGCTGTATAGATTTTGGTCTGTCGCGGTGATCT	814
Db	696	GTGTGTAATCTCTTCTACATCTACTGACAGCTATGATATGTTGGTCACTGCGTTGATTTT	755
OY	815	CATGAACCTATGATAGAAACCTTTGTTGGTGGAAAAAGATCATGTRACATCAATACG	874
Db	756	CATGAATTAATGACAGAAAGCCTCTGTTTCTCGGTAGAGATCATGTRCAACACACTACG	815
OY	875	CTTGTTAACGAGCTTCTTGGACCCCAACAGAGGTGATTTGGCTCTCTCCAAATAGA	934
Db	816	CTGTCTTATGAGAGTTGATTTGGACACCCCATTTGAGGCTGAAATGGAGTTCT--GAAAGA	872
OY	935	AGATGCAAAAGATACATCAGGCACTCCACCAACATCTCCGACAGACTTTAGCAGAAGT	994
Db	873	GAAATGCAAAAGGTRACATCAGACAGGTCTCTTTACGTCGACATCATTTGTGAAAA	932
OY	995	TTTCCCTCATGTGAACCATTTGGCTATGATCTTTCGATATAAATGTTGACATTTGCATC	1054
Db	933	GTTTCCACACGCTAAACCTCCCTCCCTCATTTGATCTTTGTAAGAAAAATGTTGACATTTGATCC	992
OY	1055	TACTAGAAAGATTTACGTTGAGAGACATTAATCATCTACCTCTGCAAAACCTCCACAGA	1114
Db	993	CAGAAGAGACTTACTTGTAGAACGCGCTGACACATCTTACTACATACATGCTTCAATGA	1052
OY	1115	TGCAGGTGACAGACCGATCTGCCCTGTTCATTTCTCTTTGACTTTGAGACCAAGAGAT	1174
Db	1053	TATTAGTAGACAGCGCTTTTGGACAGACTCCTTTTACTCTCGATTTTGAACACAGATGCT	1112
OY	1175	AGAGAAAGACGAATTTAAGACATGATATATCAGGAAAGCTTTGTCACTGATATCTCGAATA	1234
Db	1113	TACTAGGAAGCAAAATGAAAGGTGATTTACAGGAGGCGCTTGCAATTTAAACCCGAATA	1172

GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:49:16 ; Search time 406 Seconds
(without alignments)
9568.219 Million cell updates/sec

Title: US-09-623-034-1
1725
Sequence: 1 tatatatacaccatgtctca.....gagcaagaagactgtgtata 1725

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	100.0	1725	18	AAT60349
2	1320	76.5	1786	18	AAT60350
3	552	32.0	1544	19	AAV27563
4	534	31.0	1197	22	AAC84262
5	533.4	30.9	1197	22	AAC84265
6	531.8	30.8	1188	21	AAC43105
7	494	28.6	1125	22	AAC84259
8	489.2	28.4	1525	21	AAC44071
9	471	27.3	1546	21	AAC43674

10	470.6	27.3	1451	21	AAC32826	Arabidopsis thalia
11	468.6	27.2	1119	22	AAC84253	Signal transductio
12	445.2	25.8	1282	21	AAC33580	Arabidopsis thalia
13	445.2	25.8	1359	21	AAC47261	Arabidopsis thalia
14	438.6	25.4	1116	21	AAC48312	Arabidopsis thalia
15	420	24.3	1718	24	ABA91076	Physcomitrella pat
16	416.4	24.1	1122	21	AAC42749	Arabidopsis thalia
17	378	21.9	1065	21	AAC42861	Arabidopsis thalia
18	337.2	19.5	1113	21	AAC43076	Arabidopsis thalia
19	335.6	19.5	1615	21	AAC48068	Zea mays DNA fragm
20	331.6	19.2	1138	21	AAZ98356	A. thaliana gene 1
21	330.8	19.2	1113	22	AAC84256	Signal transductio
22	330.8	19.2	1654	21	AAC44676	Zea mays DNA fragm
23	329.8	19.1	1131	21	AAC51150	Arabidopsis thalia
24	306.4	17.8	1307	21	AAC42374	Arabidopsis thalia
25	301.2	17.5	1719	21	AAC48025	Zea mays DNA fragm
26	298	17.3	1110	22	AAC84250	Signal transductio
27	294.4	17.1	953	24	ABA91063	Physcomitrella pat
28	289.6	16.8	1086	21	AAC42874	Arabidopsis thalia
29	265.2	15.4	1957	20	AAK86361	CDNA encoding mito
30	262	15.2	1770	21	AAC49947	Arabidopsis thalia
31	254	14.7	1627	22	AAH22558	P. patens MPK-1 en
32	248.6	14.4	1524	21	AAC41619	Arabidopsis thalia
33	247	14.3	1731	21	AAC45785	Arabidopsis thalia
34	246.6	14.3	2257	22	AAC4274	Signal transductio
35	244.2	14.2	1785	21	AAC42701	Arabidopsis thalia
36	244.2	14.2	1950	21	AAC45953	Arabidopsis thalia
37	233.6	13.5	1879	21	AAC49789	Arabidopsis thalia
38	233	13.5	1467	13	AAQ20261	ERK2. Rat ratus.
39	233	13.5	1815	19	AAV71031	Green fluorescent
40	233	13.5	1818	19	AAV71023	Signal transductio
41	232.8	13.5	1635	22	AAC84283	Human CSAID bindin
42	232	13.4	1100	20	AAZ11605	DNA encoding novel
43	232	13.4	3757	23	AAK8119	Human cDNA differe
44	232	13.4	3757	24	ABK8381	Human CSAID bindin
45	232	13.4	3774	20	AAZ11601	

ALIGNMENTS

RESULT 1
AAT60349
ID AAT60349 standard: CDNA to mRNA; 1725 BP.

AC AAT60349;
XX
XX
04-JUN-1997 (first entry)
DT
XX
XX
DE MAP kinase #1 coding sequence.
KW Mitogen activated protein kinase; MAP; infectious specific protein;
KW plant; jasmon acid; ss.
XX
XX
OS Synthetic.
PN JP09065881-A.
XX
XX
PD 11-MAR-1997.
XX
XX
PF 29-AUG-1995; 95JP-0220935.
XX
XX
PR 29-AUG-1995; 95JP-0220935.

(NORU) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
WPI: 1997-220416/20.
DR P-PSDB: AAM15512.
XX
XX
PT Wound-stress inducible MAP kinase - used to regulate the synthesis
PT of jasmon acid
XX
XX
PS Claim 5; Page 11-13; 21pp; Japanese.

XX AAT60349 and AAT60350 represent the coding sequences for the mitogen
 CC activated protein (MAP) kinases of the invention. The protein encoded
 CC by this sequence contains the T-E-Y sequence, in which the threonine and
 CC tyrosine residues are phosphorylated to activate the protein at residues
 CC 201-203. The MAP kinase and its gene can be used to regulate the
 CC synthesis of jasmonate acid and the synthesis of a group of infectious
 CC specific proteins. By introducing the MAP kinase gene into a plant,
 CC thereby inducing expression of the mRNA for MAP kinase (or its antisense
 CC RNA), the synthesis of jasmonate acid and a group of infectious specific
 CC proteins can be regulated in the plant.

XX Sequence 1725 BP; 469 A; 361 C; 326 G; 569 T; 0 other;

Query Match 100.0%; Score 1725; DB 18; Length 1725;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1725; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATATATACATATGCTCATATTTACACTTATTACATGTCATATGATCTGCTTAAAT 60
 Db 1 TATATATACATATGCTCATATTTACACTTATTACATGTCATATGATCTGCTTAAAT 60
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 QY 121 ATGCATAATGGGTGCGGAGAGTCAATCCCTGATTTTCTCGGTTTAACTGACG 180
 Db 121 ATGCATAATGGGTGCGGAGAGTCAATCCCTGATTTTCTCGGTTTAACTGACG 180
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 Db 181 GCGACATATATGTCAGTTGATATTTTGGTAATTTCTTGAATCACTACCAAGATC 240
 QY 241 GTCTCTATATATGCTATTTGCTGCTGATGATGAAATGTCGCGGTTTGATA 300
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 Db 481 CTACTGAACCTGATGATCTGATCTTCAACAAATTAATTAATCAACCAAGTTTATCAG 540
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 Db 541 AGAGTCACTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 600
 QY 601 CGAATGTTCTTCATAGAGATCTCAAAACGAGCACTTTTGGTAAATGCAAAATTTGTATC 660
 Db 601 CGAATGTTCTTCATAGAGATCTCAAAACGAGCACTTTTGGTAAATGCAAAATTTGTATC 660
 QY 661 TTAAGATATGATGCTTGGTCTGCTAGGCCAAACATAGAGACGAGAAATGAGCGAAT 720
 Db 661 TTAAGATATGATGCTTGGTCTGCTAGGCCAAACATAGAGACGAGAAATGAGCGAAT 720
 QY 721 ATGTTGTAACAGATGCTGACAGGACAGAGCTTTTGTGTAATCTTCAGATTAACAGT 780
 Db 721 ATGTTGTAACAGATGCTGACAGGACAGAGCTTTTGTGTAATCTTCAGATTAACAGT 780
 QY 781 CTGCTATAGATGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
 Db 781 CTGCTATAGATGTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

QY 841 TGTGGTGGAAAAAGATCATGATCATCAATACGCTTGTAAACGAGCTTCTTGGCACCC 900
 Db 841 TGTGGTGGAAAAAGATCATGATCATCAATACGCTTGTAAACGAGCTTCTTGGCACCC 900
 QY 901 CAACAGAGCTGATCTTGGCTTCTCCAAATGATGCAAGAGATACATGAGCAAC 960
 Db 901 CAACAGAGCTGATCTTGGCTTCTCCAAATGATGCAAGAGATACATGAGCAAC 960
 QY 961 TCCACAAACATCCCGCAGCAGTATGACAGAGTTTCCCTCATGTGACCATTTGGCTA 1020
 Db 961 TCCACAAACATCCCGCAGCAGTATGACAGAGTTTCCCTCATGTGACCATTTGGCTA 1020
 QY 1021 TTGATCTTGTGATTAATGTTGATGATGATCTGATCTGATGATGATGATGATGATG 1080
 Db 1021 TTGATCTTGTGATTAATGTTGATGATGATCTGATCTGATGATGATGATGATGATG 1080
 QY 1081 CATTAATGATCTCTACCTTCCAAAGCTCCACGATGAGAGTGAAGCAACGATCTGCCCTG 1140
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 QY 1141 TTCCATCTCTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200
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 QY 1381 AAGCAGCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 Db 1381 AAGCAGCCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440
 QY 1441 TGTCTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
 Db 1441 TGTCTGTGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1500
 QY 1501 CAGCACAACATTTATATCTCCCATCTATCTATGATTTGATCTTGTGATGATGATG 1560
 Db 1501 CAGCACAACATTTATATCTCCCATCTATCTATGATTTGATCTTGTGATGATGATG 1560
 QY 1561 AGCTAAACCAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
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 QY 1621 CAAGTTCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 Db 1621 CAAGTTCTCTTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
 QY 1681 TTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1725
 Db 1681 TTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1725

RESULT 2
 AAT60350
 ID AAT60350 standard; cDNA to mRNA; 1786 BP.

XX AAT60350;

XX 04-JUN-1997 (first entry)

XX MAP kinase #2 coding sequence.

XX Mitogen activated protein kinase; MAP; infectious specific protein;

KW plant; jasmonic acid; ss.
XX Synthetic.
OS
XX JP09065881-A.
FN
XX
PD 11-MAR-1997.
XX
PE 29-AUG-1995; 95JP-0220935.
XX
PR 29-AUG-1995; 95JP-0220935.
XX
PA (NORO) NORINSUISANSO NOGYO SEIBUTSU SHIGEN.
XX
DR WPI: 1997-220416/20.
XX P-PSDB: AAM1513.
XX
PT Wound-stress inducible MAP kinase - used to regulate the synthesis
XX of jasmonic acid
XX
PS Disclosure: Page 14-16; 21pp; Japanese.
XX
CC AAT60349 and AAT60350 represent the coding sequences for the mitogen
CC activated protein (MAP) kinases of the invention. The protein encoded
CC by this sequence contains the T-E-Y sequence, in which the threonine and
CC lysine residues are phosphorylated to activate the protein at residues
CC 249-251. The MAP kinase and its gene can be used to regulate the
CC synthesis of jasmonic acid and the synthesis of a group of infectious
CC specific proteins. By introducing the MAP kinase gene into a plant,
CC thereby inducing expression of the mRNA for MAP kinase (or its antisense
CC RNA), the synthesis of jasmonic acid and a group of infectious specific
CC proteins can be regulated in the plant.
XX
XX Sequence 1786 BP; 503 A; 390 C; 353 G; 540 T; 0 other;

Query Match 76.5%; Score 1320; DB 18; Length 1786;
Best Local Similarity 99.0%; Pred. No. 0;
Matches 1342; Conservative 0; Mismatches 5; Indels 9; Gaps 1;

QY 206 TTTTGGTAAATTTCTTTGATGACACACAGATAGCTCCCTCTATATGCGTATGTCG 265
DB 440 TTTTGGTAAATTTCTTTGATGACACACAGATAGCTCCCTCTATATGCGTATGTCG 499
QY 266 TGGTCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 325
DB 500 TGGTCTTATGGAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 559
QY 326 TAAAGAAATCGCGAATGCGTTGATATTTACATGATGATCTAAGAGACTCTCCGTGAGAT 385
DB 560 TAAAGAAATCGCGAATGCGTTGATATTTACATGATGATCTAAGAGACTCTCCGTGAGAT 619
QY 386 TAAAGTCTCTCGCCCATTTAGACCATGAAATGTAATGTTTAAAGACGCTGATCTCC 445
DB 620 TAAAGTCTCTCGCCCATTTAGACCATGAAATGTAATGTTTAAAGACGCTGATCTCC 670
QY 446 ACCCTTACGAGAGAGATTTCTGATGTTTACATGCTCTACTGAACTGATGATGATGAT 505
DB 671 ACCCTTACGAGAGAGATTTCTGATGTTTACATGCTCTACTGAACTGATGATGATGAT 730
QY 506 TCACCAATTAATTAAGATCAACCAAGTTTATCAGAGAGATCAGTCTGATCTGATCA 565
DB 731 TCACCAATTAATTAAGATCAACCAAGTTTATCAGAGAGATCAGTCTGATCTGATCA 790
QY 566 TCAGTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
DB 791 TCAGTCTCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 850
QY 626 ACCGAGCAACCTTTGATGATGCAAAATTTGATCTTAAGATGATGATGATGATGATGAT 685
DB 851 ACCGAGCAACCTTTGATGATGCAAAATTTGATCTTAAGATGATGATGATGATGATGAT 910
QY 686 TAGGCGCAAAATTAAGAGAAAGAAATATGAGCAATATATGTTTAAACAGATGATGATGAT 745
DB 745 TAGGCGCAAAATTAAGAGAAAGAAATATGAGCAATATATGTTTAAACAGATGATGATGAT

DB 911 TAGGCCAAACATAGAGAAAGAAATATGAGCAATATGTTTAAACAGATGATGATGATGAT 970
QY 746 ACCGAGCTTTGTTGAACTCTTCGATTTACATCTCTCTATAGATGTTTGGTCTGTCGG 805
DB 971 ACCGAGCTTTGTTGAACTCTTCGATTTACATCTCTCTATAGATGTTTGGTCTGTCGG 1030
QY 806 TTGCATCTTCAATGAACTTTATGATGAAACCTTTGTTGGTGGAAAGATCATGTACA 865
DB 1031 TTGCATCTTCAATGAACTTTATGATGAAACCTTTGTTGGTGGAAAGATCATGTACA 1090
QY 866 TCAATATACGCTTTGTTAACGAGCTTTTGGCAACCCCAACAGAGCTGATCTTGGCTCT 925
DB 1091 TCAATATACGCTTTGTTAACGAGCTTTTGGCAACCCCAACAGAGCTGATCTTGGCTCT 1150
QY 926 CCAAAATGAGATGCAAAAGATATCATAGGCACTCCCAACATCTCTGCGCAGAGATT 985
DB 1151 CCAAAATGAGATGCAAAAGATATCATAGGCACTCCCAACATCTCTGCGCAGAGATT 1210
QY 986 AGCAGAGTTTTCCTCATGTAACCCCATTTGGCTATGATCTTGGCTGATGATGATGATGAT 1045
DB 1211 AGCAGAGTTTTCCTCATGTAACCCCATTTGGCTATGATCTTGGCTGATGATGATGAT 1270
QY 1046 ATTGATCTTACTAGAAATTTACAGTTGAGGAACATTAGATCATCTCTCTCTGCAAA 1105
DB 1271 ATTGATCTTACTAGAAATTTACAGTTGAGGAACATTAGATCATCTCTCTCTGCAAA 1330
QY 1106 GCTCAGCATGAGGTGACGAACGATCTGCTCTTCTCATCTTCTCTGATTTGAGCA 1165
DB 1331 GCTCAGCATGAGGTGACGAACGATCTGCTCTTCTCATCTTCTCTGATTTGAGCA 1390
QY 1166 ACAAGATATGAGAAAGCAAAATTTAAGACATGATATATCAGAAAGCTTTGCTACTGAA 1225
DB 1391 ACAAGATATGAGAAAGCAAAATTTAAGACATGATATATCAGAAAGCTTTGCTACTGAA 1450
QY 1226 TCTGATATGCTTAAACATTAAGAAATCAATCTTCTCTCTGTTTCCCTTGTGATC 1285
DB 1451 TCTGATATGCTTAAACATTAAGAAATCAATCTTCTCTCTGTTTCCCTTGTGATC 1510
QY 1286 TGGATATCTACTCTTCCAGCTGATGATTTCTGCTGAGCGAGCACTCAATGTTT 1345
DB 1511 TGGATATCTACTCTTCCAGCTGATGATTTCTGCTGAGCGAGCACTCAATGTTT 1570
QY 1346 GCTCAGCTGAGTCTTTCGCAACTTGTATGTAAGCAAGCTTCAATGTCAGCAT 1405
DB 1571 GCTCAGCTGAGTCTTTCGCAACTTGTATGTAAGCAAGCTTCAATGTCAGCAT 1630
QY 1406 CTATATATCTTTTATTTTATTTTATTTAATGAGTGTCTGTGAGTACTTGTGAGCA 1465
DB 1631 CTATATATCTTTTATTTTATTTTATTTAATGAGTGTCTGTGAGTACTTGTGAGCA 1690
QY 1466 CCTGATATTTTATTTGATATTTGTAACCTCCCGCAGACACATTTATATCTCCAC 1525
DB 1691 CCTGATATTTTATTTGATATTTGTAACCTCCCGCAGACACATTTATATCTCCAC 1750
QY 1526 TCATCTTATGATTTGTAATCTTGTGTTGATTTCA 1561
DB 1751 TCATCTTATGATTTGTAATCTTGTGTTGATTTCA 1786

RESULT 3
AAV27563
ID AAV27563 standard; cDNA; 1544 BP.
XX
AC AAV27563;
DB
DT 22-SEP-1998 (first entry)
XX
DE Salicylic acid induced MAP kinase encoding cDNA.
XX
XX Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
KW Salicylic acid induced protein; SIP; mitogen-activated protein; MAP;
KW tobacco; disease resistance; microbial pathogen; MAP kinase; ds.
XX
OS Nicotiana sp.

XX Key Location/Qualifiers
 FH 129.1310
 FT CDS /*tag= a
 FT /product= "salicylic acid induced MAP kinase"
 XX
 XX MO9818939-A1.
 XX
 XX 07-MAY-1998.
 XX
 XX 24-OCT-1997; 97MO-US19219.
 XX
 XX 21-APR-1997; 97US-0837593.
 XX 25-OCT-1996; 96US-0029805.
 XX
 XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
 XX
 XX Kiessig DF, Zhang S;
 XX MPI; 1998-272230/24.
 XX P-SDB; AAM61252.
 XX
 XX Salicylic acid induced MAP kinase - obtained from tobacco, used to
 PT produce plants having increased disease resistance, against e.g.
 PT microbial pathogens
 XX
 XX Claim 11; Pages 21-22; 97pp; English.
 XX
 XX This cDNA encodes a salicylic acid induced protein (SIP) kinase. This SIP
 CC kinase is an unique member of the mitogen-activated protein (MAP) kinase
 CC family. The salicylic acid induced MAP kinase of the invention comprises
 CC kinase subdomains I to XI of serine/threonine kinases. The protein is
 CC activated by an agent that induces a disease defence response in plants
 CC by way of a signal transduction pathway that is at least partially
 CC dependent on salicylic acid. Host plant cells transformed with a vector
 CC containing a recombinant DNA molecule encoding the salicylic acid induced
 CC MAP kinase is used to produce the protein recombinantly. The products can
 CC be used to produce plants with increased disease resistance. The products
 CC may also be used as a research tool to identify other proteins involved
 CC in the hypersensitive response and systemic acquired response in plants.
 CC
 XX Sequence 1544 BP; 449 A; 294 C; 335 G; 466 T; 0 other;
 SO
 Query Match 32.0%; Score 552; DB 19; Length 1544;
 Best Local Similarity 70.1%; Pred. No. 1; Le-138;
 Matches 757; Conservative 0; Mismatches 320; Indels 3; Gaps 1;

DB 581 TATTCGCTTAATCAGGGTTATCTGAGAGACACTGCTAGTATTTCTGTATGATGATCCT 640
 QY 575 CCGTGGCCCTAAAPACATACATTCGGAGATGTTCTTCATAGAGATCTCAACCGAGCA 634
 DB 641 CCGAGGTTAAATACATACATTTCTGGAATGTTCTGACAGAGGACTTGAAGCTTGACAA 700
 QY 635 CATTGCTAAATGCAAAATGATCTTAAAGATATGTGACTTTGGTCTAGGCCAA 694
 DB 701 TCTCCTGTGAATGCCAACTGTGATTTAAAGATATGATTTGGCTACTGCTGAC 760
 QY 695 CATAGAGAACAGATATGAGGAATATGTTGTAACAGATGTTAGAGGACACAGAGCT 754
 DB 761 TTCTGAACATGCTATTATGAGGAATATGTTGACAGATGTTATGCTACCTGAGCT 820
 QY 755 TTGTTGAACTCTTCAATATACACTGCTGCTATAGATGTTGCTGCTGCTGCTGCT 814
 DB 821 GTTGTAAATTCGCTGACATATCTGAGCAATTTGACATGCTGAGTGGCTGCAATTT 880
 QY 815 CATGGAACCTTAATGAAATGAAACCTTTGTTGGTGAAGAAATCATGATCATCAATACG 874
 DB 881 CATGGAATGATGAGACAGAAACCCCTATTTCTGTTAGATACAGTACACACAGCTGCG 940
 QY 875 CTTCCTAACGAGCTTCTTGGCAACCCCAAGAAAGCTGATCTTGGCTCTCCAAATGA 934
 DB 941 TCTTATTATGAGCTGATTTGGTGTACTCTCTCAGAGGCTGAATGAGATTTT---AAATGA 997
 QY 935 AGATGCAAGAGATACATACAGCAACTGCCCAACATCTCGCAGAGCTTACAGAGT 994
 DB 998 GATGCAAAACGATACATACCTCGCCCACTCTCTTACCGTACGAAATCATCTACTGAA 1057
 QY 995 TTTCCTCAGTGAACCCATTTGCTATGATCTTGTGCAATGTTGATTCATTCGATCC 1054
 DB 1058 GTTCCACATGATCACCCCACTGCAATGATCTGTCGAAATGCTGACATTTGATTC 1117
 QY 1055 TACTAGAGAAATACAGTTGAGGAAGCATGATGATCATCTTACCTGCAAGATCCACGA 1114
 DB 1118 TAGAAGAGAAATACATTAAGGTGACATCTTCACTTACCTGACATCGCTCCACGA 1177
 QY 1115 TGCAGGTGAGAACCCATCTGCCCTGTTCCATTTCTTGTGATTTGAGCAAGCAAT 1174
 DB 1178 TATATGAGAGAGCCATTTGACATGACTCCCTTAGCTTGACATTTGACAGATGCCCT 1237
 QY 1175 AGGAGAAAGCAATTAAGACATGATATATCAGAAAGCTTTGCTACTGATCTGATA 1234
 DB 1238 TACGAGAGAACATGAGAGAGCTGATTTACAGGAGCTGCTTGCATTTAATCTGATA 1297
 RESULT 4
 AAC84262
 ID AAC84262 standard; cDNA; 1197 BP.
 AAC84262:
 AC 19-MAR-2001 (first entry)
 DT
 XX Signal transduction protein encoding cDNA.
 DE
 XX Zea mays; maize; signal transduction protein; phytohormone; ethylene;
 KM auxin; cytokinin; gibberellin; immunogen; ss.
 OS
 XX Zea mays.
 OS
 XX
 XX Key Location/Qualifiers
 FH 1..1197
 FT CDS /*tag= a
 FT /product= "signal transduction protein"
 XX
 XX WO200070059-A2.
 XX
 XX 23-NOV-2000.
 XX
 XX 28-APR-2000; 2000MO-US11687.
 XX

XX (PION-) PIONEER HI-BRED INT. INC.
 PA Helentjaris TG;
 XX WPI; 2001-031929/04.
 DR P-PSDB; AAB48048.
 XX
 PT New signal transduction nucleic acids and encoded proteins useful for
 PT regulating phytohormone expression, including ethylene, auxins,
 PT cytokinins and gibberellin, to provide control of plant response to
 PT environmental stresses.
 XX
 XX Claim 1: Page 95-96; 126pp; English.
 CC The invention provides a means for signal transduction proteins and encoding
 CC nucleotide sequences. The nucleic acids are useful for regulating
 CC expression of phytohormones, including ethylene, auxins, cytokinins,
 CC and gibberellin, to effect developmental changes in plants and provide
 CC control of plant response to environmental stresses. They may also be
 CC used as probes or amplification primers in the detection, quantitation or
 CC isolation of gene transcripts, for detecting mutations in the gene, for
 CC monitoring upregulation of expression or changes in enzyme activity in
 CC screening assays of compounds, for detection of any number of allelic
 CC variants, or for site-directed mutagenesis in eukaryotic cells. They may
 CC further be used for recombinant expression of their encoded polypeptides,
 CC as immunogens in the preparation or screening of antibodies, and in sense
 CC or antisense suppression of genes in a host cell, tissue or plant. The
 CC proteins may be used in assays for enzyme agonists or antagonists, as
 CC immunogens or antigens to obtain antibodies specifically immunoreactive
 CC with the proteins. The present sequence represents a cDNA encoding a
 CC signal transduction protein of the invention.
 XX
 SQ Sequence 1197 BP; 317 A; 306 C; 281 G; 293 T; 0 other;
 Query Match 30.94; Score 533.4; DB 22; Length 1197;
 Best Local Similarity 69.58; Pred. No. 1e-133;
 Matches 739; Conservative 0; Mismatches 321; Indels 3; Gaps 1;

Db 611 ACTGTGACCTTCAGATATGATATGTTGGGCTTGCTCGCACCACCCTCAGAAATGATTTTA 670
 QY 712 TGACGSAATATGTTGTACACGATGTACAGGACGACGAGCTTTGTTGAATCTTCAG 771
 Db 671 TGACTGAATATGTTGTTCACAGATGTATAGACGACGAGCTTTTATGAACTCCTCG 730
 QY 772 ATTACACTGCTGTATAGATGTTGGTCTGTGCTGGTTGCATCTTCAGAACTTATGATA 831
 Db 731 AATATACTGCTGCATGATGT 790
 QY 832 GAAACCTTTTGT 891
 Db 791 GAAACCTTTTGT 850
 QY 892 TTGGACCCCAAGAGAGCTGATCTTGCTTCCTCCAAATGAAGATCAAGATACA 951
 Db 851 TTGGAACACCCAAATGAGGCTGATCTTGCTTCCTCCAAATGAAGATACA 907
 QY 952 TCAGGCAACCTCCCAACATCTCTGCGCAGCAGTAGAGAAATTTTCCTCTGTAAC 1011
 Db 908 TCGGCAACCTCCCTGTCATCTGACAGAGCTCTTCCGAAATTTCCACATGTACAC 967
 QY 1012 CATTGCTATTGATCTTGTGATTAATGTTGACATTCGATCTTCTAAGAAATTTACAG 1071
 Db 968 CTTTAGCAATTTGACCTATGTGTGAAAGATGCTTACTTTGATCTTACAGAAATTA 1027
 QY 1072 TTGAGGAAGCTTTGATGATCATCTACCTTGCAAGCTCCAGATGACAGTACGACGA 1131
 Db 1028 TTGAAGGCGCACTTGCACACCTTACTTGGCATCTTCAATGATAGTATAGCCAG 1087
 QY 1132 TCTGCTGTTTCCATCTTCTCTTACCTTGTAGCAACAAGAAATGAGAGCAAAATTA 1191
 Db 1088 TCTGCTCAATGCTCTTCACTGAGCTTGCAGCTCGACAGCATGCTTATCTGAAAGACAGATGA 1147
 QY 1192 AGGACATGATATATACGGAACCTTGTACAGAAATTCGATTA 1234
 Db 1148 AGGATGATCTACCAAGAGGCTCTTGCATTCACCAAGATTA 1190

RESULT 6
 ID AAC43105
 XX AAC43105;
 AC 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38047.
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126284.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999;	99US-0130510.
PR 23-APR-1999;	99US-0130891.
PR 28-APR-1999;	99US-0131449.
PR 30-APR-1999;	99US-0132048.
PR 30-APR-1999;	99US-0132407.
PR 04-MAY-1999;	99US-0132484.
PR 05-MAY-1999;	99US-0132485.
PR 06-MAY-1999;	99US-0132486.
PR 07-MAY-1999;	99US-0132487.
PR 11-MAY-1999;	99US-0132863.
PR 14-MAY-1999;	99US-0134256.
PR 14-MAY-1999;	99US-0134218.
PR 14-MAY-1999;	99US-0134219.
PR 14-MAY-1999;	99US-0134321.
PR 18-MAY-1999;	99US-0134370.
PR 18-MAY-1999;	99US-0134768.
PR 19-MAY-1999;	99US-0134941.
PR 20-MAY-1999;	99US-0135124.
PR 21-MAY-1999;	99US-0135353.
PR 24-MAY-1999;	99US-0135629.
PR 25-MAY-1999;	99US-0136021.
PR 27-MAY-1999;	99US-0136392.
PR 28-MAY-1999;	99US-0136782.
PR 01-JUN-1999;	99US-0137222.
PR 03-JUN-1999;	99US-0137528.
PR 04-JUN-1999;	99US-0137502.
PR 07-JUN-1999;	99US-0137724.
PR 08-JUN-1999;	99US-0138094.
PR 10-JUN-1999;	99US-0138540.
PR 10-JUN-1999;	99US-0138847.
PR 14-JUN-1999;	99US-0139119.
PR 16-JUN-1999;	99US-0139452.
PR 17-JUN-1999;	99US-0139492.
PR 18-JUN-1999;	99US-0139459.
PR 18-JUN-1999;	99US-0139460.
PR 18-JUN-1999;	99US-0139461.
PR 18-JUN-1999;	99US-0139462.
PR 18-JUN-1999;	99US-0139463.
PR 18-JUN-1999;	99US-0139458.
PR 18-JUN-1999;	99US-0139459.
PR 18-JUN-1999;	99US-0139460.
PR 23-JUN-1999;	99US-0139889.
PR 23-JUN-1999;	99US-0140353.
PR 23-JUN-1999;	99US-0140354.
PR 24-JUN-1999;	99US-0140695.
PR 28-JUN-1999;	99US-0140823.
PR 29-JUN-1999;	99US-0140991.
PR 30-JUN-1999;	99US-0141287.
PR 01-JUL-1999;	99US-0141847.
PR 01-JUL-1999;	99US-0142154.
PR 02-JUL-1999;	99US-0142055.
PR 06-JUL-1999;	99US-0142390.
PR 08-JUL-1999;	99US-0142803.
PR 09-JUL-1999;	99US-0142920.
PR 12-JUL-1999;	99US-0142977.
PR 13-JUL-1999;	99US-0143542.
PR 14-JUL-1999;	99US-0143624.
PR 15-JUL-1999;	99US-0144005.
PR 16-JUL-1999;	99US-0144085.
PR 16-JUL-1999;	99US-0144086.
PR 19-JUL-1999;	99US-0144325.
PR 19-JUL-1999;	99US-0144331.
PR 19-JUL-1999;	99US-0144332.
PR 19-JUL-1999;	99US-0144333.
PR 19-JUL-1999;	99US-0144334.
PR 19-JUL-1999;	99US-0144335.
PR 20-JUL-1999;	99US-0144352.

PR 20-JUL-1999;	99US-0144632.
PR 20-JUL-1999;	99US-0144684.
PR 21-JUL-1999;	99US-0144814.
PR 21-JUL-1999;	99US-0145088.
PR 21-JUL-1999;	99US-0145088.
PR 22-JUL-1999;	99US-0145087.
PR 22-JUL-1999;	99US-0145089.
PR 22-JUL-1999;	99US-0145192.
PR 23-JUL-1999;	99US-0145145.
PR 23-JUL-1999;	99US-0145218.
PR 26-JUL-1999;	99US-0145224.
PR 27-JUL-1999;	99US-0145913.
PR 27-JUL-1999;	99US-0145918.
PR 27-JUL-1999;	99US-0145919.
PR 28-JUL-1999;	99US-0145951.
PR 02-AUG-1999;	99US-0146386.
PR 02-AUG-1999;	99US-0146388.
PR 03-AUG-1999;	99US-0147038.
PR 04-AUG-1999;	99US-0147204.
PR 05-AUG-1999;	99US-0147302.
PR 05-AUG-1999;	99US-0147192.
PR 06-AUG-1999;	99US-0147260.
PR 06-AUG-1999;	99US-0147303.
PR 09-AUG-1999;	99US-0147416.
PR 09-AUG-1999;	99US-0147493.
PR 10-AUG-1999;	99US-0147935.
PR 11-AUG-1999;	99US-0148171.
PR 12-AUG-1999;	99US-0148319.
PR 13-AUG-1999;	99US-0148565.
PR 16-AUG-1999;	99US-0148684.
PR 17-AUG-1999;	99US-0149175.
PR 18-AUG-1999;	99US-0149426.
PR 20-AUG-1999;	99US-0149722.
PR 20-AUG-1999;	99US-0149722.
PR 20-AUG-1999;	99US-0149722.
PR 23-AUG-1999;	99US-0149929.
PR 23-AUG-1999;	99US-0149930.
PR 25-AUG-1999;	99US-0150566.
PR 26-AUG-1999;	99US-0150884.
PR 27-AUG-1999;	99US-0151065.
PR 27-AUG-1999;	99US-0151066.
PR 27-AUG-1999;	99US-0151080.
PR 30-AUG-1999;	99US-0151303.
PR 31-AUG-1999;	99US-0151438.
PR 01-SEP-1999;	99US-0151930.
PR 07-SEP-1999;	99US-0152363.
PR 10-SEP-1999;	99US-0153070.
PR 13-SEP-1999;	99US-0153758.
PR 15-SEP-1999;	99US-0154018.
PR 16-SEP-1999;	99US-0154039.
PR 20-SEP-1999;	99US-0154779.
PR 22-SEP-1999;	99US-0155139.
PR 23-SEP-1999;	99US-0155486.
PR 24-SEP-1999;	99US-0155659.
PR 28-SEP-1999;	99US-0156458.
PR 29-SEP-1999;	99US-0156596.
PR 04-OCT-1999;	99US-0157117.
PR 05-OCT-1999;	99US-0157753.
PR 06-OCT-1999;	99US-0157865.
PR 07-OCT-1999;	99US-0158029.
PR 08-OCT-1999;	99US-0158232.
PR 12-OCT-1999;	99US-0158369.
PR 13-OCT-1999;	99US-0159293.
PR 13-OCT-1999;	99US-0159294.
PR 13-OCT-1999;	99US-0159295.
PR 14-OCT-1999;	99US-0159329.
PR 14-OCT-1999;	99US-0159330.
PR 14-OCT-1999;	99US-0159331.

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PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160880.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match 30.8%; Score 531.8; DB 21; Length 1188;
 Best Local Similarity 69.0%; Pred. No. 2,7e-133;
 Matches 744; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

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QY 157 ATTTCTCTGGGTTTAACTCAGCGGACAAATATGATACAGTTTATTTGGTAT 216
DB 104 ATATTCGGGACTCTTATCCATGATGATGATGATGATGATGATGATGATGAT 163
QY 217 TCTTGAATCATTACCAAGATATGCTCTCTATATGCTTATGCTGATGCTAT 276
DB 164 TCTTGAAGTCCAGCGGATTAAGATTAAGCGATGATGATGATGATGATGATGAT 223
QY 277 GAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 336
DB 224 GCATCGGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 283
QY 337 CGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 396
DB 284 CTAAACGCTTTTGAACATTAAGTTATGCTGATGATGATGATGATGATGATGAT 343
QY 397 GCAATTAAGCAATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 456
DB 344 GTCACTGATGATGAATGATGATGATGATGATGATGATGATGATGATGATGAT 403
QY 457 GGGAGTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 516
DB 404 ACGCTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 463
QY 517 TTAGATCAACCAAGGTTTATCAGAGATCAGTCACTGATGATGATGATGATGAT 576
DB 464 TTGGGTCAATCAAGCATATATCCAGAGACATTCAGATATTTCTTACAGATCTCC 523
QY 577 GTGGCTTAAATATATATATATATATATATATATATATATATATATATATAT 636
DB 524 GTGATTAATATATATATATATATATATATATATATATATATATATATATAT 583
QY 637 TTTTGGTAATGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 696
DB 584 TCTCTCGAAGCAATATGATGATGATGATGATGATGATGATGATGATGATGAT 643
QY 697 TAGAGACAGAAATATATATATATATATATATATATATATATATATATATATAT 756
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QY 757 TGTGAATCTTCAATATATATATATATATATATATATATATATATATATATATAT 816
DB 704 TCTTAATCTTCTGATATATATATATATATATATATATATATATATATATATATAT 763
QY 817 TGGAACTTAATGAATAAATCTTTGTTGGTGAATAAATGATGATGATGATGATGAT 876

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DB 764 TGAATTAATGAGCGTAAAGCACTTCTCTGAGAGATCATGATCAGCTGCT 823
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QY 1057 CTAGAAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1116
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QY 1117 CAGGTGAGCAACGATGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176
DB 1061 TAAGCATGAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1120
QY 1177 GAGAAAGCAAAATTAAGCATGATATATATATATATATATATATATATATAT 1235
DB 1121 CAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179

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RESULT 7

AAC84259 standard; cDNA: 1125 BP.

AAC84259;

19-MAR-2001 (first entry)

Signal transduction protein encoding cDNA.

Zea mays; maize; signal transduction protein; phytohormone; ethylene;

auxin; cytokinin; gibberellin; immunogen; ss.

Zea mays.

Location/Qualifiers

Key 1..1125

/*tag= a

/product= "signal transduction protein"

W0200070059-A2.

23-NOV-2000.

28-APR-2000; 2000WO-US11687.

14-MAY-1999; 99US-0134282.

08-JUL-1999; 99US-0142996.

(PION-) PIONEER HI-BRED INT INC.

Helentjaris TG;

WPI; 2001-031929/04.

P-PSDB; AAB48046.

New signal transduction nucleic acids and encoded proteins useful for

regulating phytohormone expression, including ethylene, auxins,

cytokinins and gibberellin, to provide control of plant response to

environmental stresses

Claim 1; Page 89-90; 126pp; English.

The invention provides Zea mays signal transduction proteins and encoding

nucleotide sequences. The nucleic acids are useful for regulating

expression of phytohormones, including ethylene, auxins, cytokinins,

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QY	894	GGCACCCCAACAGAGAGCTGATCTTGGCTCTCTCCAAATAGAGATGCAAAAGATATAC	953
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RESULT 11
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ID AAC84253 standard; cDNA; 1119 BP.
XX
XX AAC84253;
XX
XX
DT 19-MAR-2001 (first entry)

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DE	XX		Signal transduction protein encoding cDNA.
XX	XX	Zea mays; male;	signal transduction protein; phytohormone; ethylene;
KW	auxin; cytokinin; gibberellin; immunogen; ss.		
XX	XX		
OS	Zea mays.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..1119	
FT	/tag=	a	
FT	/product=	"signal transduction protein"	
PN	WO2007/0059-AZ.		
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PD	23-NOV-2000.		
PF	28-APR-2000; 2000MO-US11687.		
PR	14-MAY-1999; 99US-0134292.		
PR	08-JUL-1999; 99US-0142996.		
XX	(PION-) PIONEER HI-BRED INT INC.		
PA			
XX	Helentjaris TG;		
PI			
DR	WPI: 2001-031929/04.		
P	P-PSDB: AAB48044.		
PT			
PT	New signal transduction nucleic acids and encoded proteins useful for		
PT	regulating phytohormone expression, including ethylene, auxins,		
PT	cytokinins and gibberellin, to provide control of plant response to		
XX	environmental stresses -		
PS			
XX	Claim 1; Page 83-85; 126pp; English.		
CC	The invention provides Zea mays signal transduction protein and encoding		
CC	nucleotide sequences. The nucleic acids are useful for regulating		
CC	expression of phytohormones, including ethylene, auxins, cytokinins,		
CC	and gibberellin, to effect developmental changes in plants and provide		
CC	control of plant response to environmental stresses. They may also be		
CC	used as probes or amplification primers in the detection, quantitation or		
CC	isolation of gene transcripts, for detecting mutations in the gene, for		
CC	monitoring upregulation of expression or changes in enzyme activity in		
CC	screening assays of compounds, for detection of any number of allelic		
CC	variants, or for site-directed mutagenesis in eukaryotic cells. They may		
CC	further be used for recombinant expression of their encoded polypeptides,		
CC	as immunogens in the preparation or screening of antibodies, and in sense		
CC	or antisense suppression of genes in a host cell, tissue or plant. The		
CC	proteins may be used in assays for enzyme agonists or antagonists, as		
CC	immunogens or antigens to obtain antibodies specifically immunoreactive		
CC	with the proteins. The present sequence represents a cDNA encoding a		
CC	signal transduction protein of the invention.		
CC			
XX			
Sequence	1119 BP; 290 A; 282 C; 268 G; 279 T; 0 other:		
Query Match	27.2%; Score 468.6; DB 22; Length 1119;		
Best Local Similarity	64.9%; Pred. No. 3.1e-116;		
Matches 693; Conservative	0; Mismatches 374; Indels 0; Gaps 0;		
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Oy	234 AAGATTCGTCCTCATATTATGCTTATTTGGTCGTGCTGCTTATGGAATGTCGTCGGT 293		
Db	109 AAGTAGCGCCCCACCATCGCGCCACATCGGTCCGGGGCTACGAGCATTTGTCCGGGGCT 168		
Oy	294 TTGATACGAGCACTGAAGAAGATGTGTGCAGTTAAGAAAATGCCGAATCGCTTATATT 353		
Db	169 GTCACTCGCATCTCAGGGAGGAGGTGTGCATCAAGAAAGTTGGCAGATCGTTCCGACAC 228		
Oy	354 TACATGGAATGCTAGAGGACCTCTCGTAGATTAAGTCTCTCCGACATTTAACCATGAA 413		

[illegible]

PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
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PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144331.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 25.8%; Score 445.2; DB 21; Length 1282;
Best Local Similarity 63.8%; Pred. No. 7e-110;
Matches 675; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 174 ACTCAGCGGAGACATATGTACAGTTGATATTTTGGTAATTCCTTGAGATCAGTACC 233
DB 78 ACACAGGGTGCCGTATGTACGACAGCTTTATGGACAACCTTTGAAGTTTCAGA 137
QY 224 AAGTATCGCTCCCTATATATGCTATTTGGTCGTGCTATTTGGAATTTGCTCGGTG 293
DB 138 AAGTATGTCCTCCCTATATGCTGTCCTATTTGGTAGAGCGCTTGCGGATTTGCTGTCGCG 197
QY 294 TTGAATACGAGCTGATGAGATGGTTCAGTTAAGAAATTCGGAATTCGTTGATATT 353
DB 198 GTGAACCTGAGTACTGAGAGAAAGTGCCTATTAAAGATTCGTAATCTTTTGATTAAC 257
QY 354 TACATGATGCTAAGAGAGACCTCCGTCGATTAAGCTCCCGCATTTTGACCATGA 413
DB 258 ATCATGATGCTAAGAGAGACCTTCGTAATAATTAACCTTCAGCATATGATCATAG 317
QY 414 AATGTAATGTTTAAAGAGAGCTGATTCCTCCACCTTACGAAGGAGTTTTCGATGT 473
DB 318 AAGCTTAAACCATCAAGAATATTTAGACCTCCGCAACGAGATATCTTCATGATGTC 377
QY 474 TACATGCTACTGAACCTCATGATGATCTTACCAAAATTAATTAATTCACCAACGAGT 533
DB 378 TACATTTGCTATGAGTTAATGAGACATGATCTTCAGCAAAATTCCTCGTTTACCAACAAATA 437
QY 534 TTATCAGAGATCACTGTCAGTACTTATCATGTATACGTCTCCCGGCGCTAAATATACATA 593

Db 438 CTGACCGATGATCGGCTTCTCTAGTATACAGCTTAAAGGGCTCAAAATACGTG 497
OY 594 CATTCGGGAATGTTCTCATAGATCTCAACCGAGACACTTTGGTAAATGCAAT 653
Db 498 CACTCGGCCAATATTCATCGATCTTAGGCCAAGCAAGCTACTTACTCGAA 557
OY 654 TGTATCTTAAGATATGACTTGTGCTTGTAGGCCAATAGAGAACAGAAATATG 713
Db 558 AACGAGCTAAAGATGATTTGGGCTTCAGAAACAACTCCGACAGACTCATG 617
OY 714 ACGAATATGTTGTAACCAATGCTACAGGCGACCAAGCTTTGTTGAATCTTCAGAT 773
Db 618 ACTAATAATGCTTACCGCTTGTACAGGGCTCTGAGTTGCTTAACTGCTCAGAG 677
OY 774 TACACTGCTATAGATGTTGGTCTGCTGCTCAATCTAGAACCTATGATATGA 833
Db 678 TACACCGCAGTATGATATTTGCTGTGTGCTGCTACCTCGGCAATATCATGCGGA 737
OY 834 AACCTTTGTTGGTGAAGAAATCATATCATCAATACCTGTTAAACCGACTTCTT 893
Db 738 CAACGCTGTTTCAGGCAAAAGATTATGTTCATCAGCTTAGGCTTAATACAGAGCTTGA 797
OY 894 GGCACCCCAACAGAACTGATCTTGGCTCTCTCCAAATGAAGATGCAAAAGATACATC 953
Db 798 GGCCTCTCAGCAATTCAGGCTCGCTCTCTGCACTGACAAAGCAAGATACGTC 857
OY 954 AGGCACTCCCAACAATCTCCGCGAGCTTACAGAAAGTTTCCCTCATGTAAACCA 1013
Db 858 AGCAAGCTCGGATACCCGAAACAGATTTGCTGTATATCCGAAATGCCCATC 917
OY 1014 TTGCTATATGATCTGTCGATTAATAATGTTGACATTCCTACTAGAAATTAAGTT 1073
Db 918 ACGGCTATCGATTTGCTGAGAGATGCTCTTTGATCTTAACCGGCTATCTCATCTC 977
OY 1074 GAGAGAGATAGATCAATCCCTACCTGCAAGCTCCAGATGAGTGAAGCAACCGATC 1133
Db 978 GATAGAGCCCTGGCCATGCTTACTATACCCGACCAATGATGAGCAAGAACCGGTC 1037
OY 1134 TGCCCTGTTCCATCTCTCTTGTGACTTTGAGCAACAGAAATAGAGCAAAATTAAG 1193
Db 1038 TGTTCGACTCTTTCAGCTTTGATTTGCAACATCTCTTTCACAGAAAGAACATTAAG 1097
OY 1194 GACATGATATATCAGAAAGCTTTGTCTACTGATCTCTGA 1231
Db 1098 GAGCTTATCTCAAGAGGTCTGCAAAATTCATCTCTGA 1135

RESULT 13
AAC47261
ID AAC47261 standard; DNA; 1359 BP.
XX AAC47261;
AC
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 53162.
XX
KM Hybridisation assay; genetic mapping; gene expression control;
XX
KW protein identification; signal transduction pathway;
XX
XX metabolic pathway; promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-01233548.

PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
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PR 29-OCT-1999: 99US-0162142.

Query Match 25.8%; Score 445.2; DB 21; Length 1359;
Best local similarity 63.8%; Pred. No. 7.1e-110;

Matches 675; Conservative 0; Mismatches 383; Indels 0; Gaps 0;

QY 174 ACTCAGCGGAGCAATATGATGACGTTGATATTTTGGTAATTTCTTGATGATCACTACC 233
DB 157 ACACACGGTGGCCGCTATGTTCACTACAACTTTATGACAACTCTTTGAAGTTCCACA 216
QY 234 AAGTATCGTCCTCTATATATGCTATTTGGTGTGCTTATGAAATGCTGCTGGTG 293
DB 217 AAGTATGCTCCCTCTATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276
QY 294 TTGAATACGAGCTGATATGATGTTGCTGACGTTAAACAAATGCGCAATGCTTGTATT 353
DB 277 GTGAACCTCAGTCTGAGAAAGGCTATTAAAGATGCGTATGCTTTGTGATAC 336
QY 354 TACATGATGCTAAGAGAGCTGCTCGGTGATTAAGCTCTCGGCACTTAGACATGAA 413
DB 337 ATCATGATGCTTAGAGAAAGCTACGTGAATTAACCTCTCAGGCATATGGATCTATGAG 396
QY 414 AATGTAATTTGTTTAAAGACGTGATTCCTCCAGCCCTTAGAAGGAGTTTCTGATGTT 473
DB 397 AAGCTATTAACCATCAAAATATTTGAAGACCTCCGCAACGAGATATCTTCATATGATGTC 456
QY 474 TACATTGCTACTGAACTACTGATGCTGATCTTACCAAAATATTTAGATCAACCAAGT 533
DB 457 TACATTGTATGATGATTAAGACACTGATCTTACCGAATCTCTCGTTCTAACCAACA 516
QY 534 TTATCAGAGATCAGTCTAGTACTGATGATGATGATGATGATGATGATGATGATGATGAT 593
DB 517 CTGACCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 576
QY 594 CATTCGCGAATGTTCTTATAGATCTCAAAACGAGCAACCTTTTGGTAAATGCAAT 653
DB 577 CACTCGGCAACATATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 636
QY 654 TGTGATCTTAAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 713
DB 637 AAGGACCTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 696
QY 714 ACGAATATGTTGTAACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 773

Db 697 ACTGAATATGCTTACCCGTTGGACAGGCTCCTGAGTTCCTTAATGCTCAGAG 756
Qy 774 TACACTGCTGATAGATGTTGGTCTGTCGTTGATCTTCAATGAACTATGATGA 833
Db 757 TACACCGAGCTATGATTTGTTGGTCTGTCGATACGCGGAATATGACGGGA 816
Qy 834 AATCCTTGTGGTGGAAAGATCATGTATCATCAATACCTGTTAAACGAGCTTCTT 893
Db 817 CAACCGTTGTTCCAGCGAAAGATTATGTTATCATGCTTAGGCTTATACAGAGCTTGA 876
Qy 894 GGCACCCCAAGAGAGCTGATCTTGGCTTCTCCAAAATGAGATGCAAGATATATC 953
Db 877 GGCCTCTCAGCAATTCAGCTCGGCTTCTTCCAGTGCACAAAGCAAGATATCCTC 936
Qy 954 AGGCACTCCCAAGAACCTCCGCGAGATAGAGAAAGTTTCCCATGTAACCA 1013
Db 937 AGGCACTCCGCGATCCCAACACAGTTTGTCTAGATTCGCAAAATGCCACT 996
Qy 1014 TTGCTATGATCTGTCGATMAATGTTGACATTCCTACTAGAGATTAACAGT 1073
Db 997 ACGCTATGATTTGCTTGAAGATGCTGCTTTGATCTTAACCGGCGATCTCATC 1056
Qy 1074 GAGGAGCATTAATCATCTCCTACCTGCAAGCTCCACGATGCAAGTGCAGAACGATC 1133
Db 1057 GATGAAGCCCTTGGCAGCTTACCTATCACCGACCATGATGCGCAAGAACCGGTC 1116
Qy 1134 TGCCCTGTCATCTCTCTTGTGACTTGAGACAGAAAGATAGAGCAATTAAG 1193
Db 1117 TGTTCGACTCTTTCAGCTTGTGATTTGCAACATCTTCTTGCACAGAAACATTAAG 1176
Qy 1194 GACATGATATATCAGAGAGCTTGTCTCACTGATCTCTGA 1231
Db 1177 GAGCTTATCTCAAGAGAGTCTGCAATTAATCAATCTCTGA 1214

RESULT 14
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AC AAC48312;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57021.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123160.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.
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OY 774 TACACTGCTATAGATGTTGTCGTGCTGCTCATCTTCATGAGAACTATATAGATA 833
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RESULT 15
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 DT 22-FEB-2002 (first entry)
 XX
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 KW Protein kinase stress-related protein; PKSRP; moss; protein kinase-6;
 KW PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9;
 KW PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-2; CK-2;
 KW casein kinase homologue-3; CK-3; mitogen-activated protein kinase;
 KW MAP kinase-2; MPK-2; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4;
 KW MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1;
 KW calcium-dependent protein kinase-2; CPK-2; overexpression;
 KW environmental stress; salinity; drought; temperature; tolerance;
 KW transgenic plant; EST; expressed sequence tag; ss.
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 OS Physcomitrella patens.
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 PN MO20017356-A2.
 PD 18-OCT-2001.
 XX
 PF 06-APR-2001; 2001WC-US11435.
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 PR 07-APR-2000; 2000US-196001P.
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Da Costa Silva EO, Bohnert HJ, Van Thielén N, Chen R;
 PI Sarria-Millan R;
 XX
 DR WPI: 2002-049153/06.
 DR P-PSDB: AAMS2837.
 XX
 PT New protein, useful for increasing tolerance to environmental stress,
 PT comprises a Protein Kinase Stress-Related Protein selected from
 PT Protein kinases, Casein kinase homologs, MAP kinases or Calcium
 PT dependent protein kinases
 XX
 PS Claim 14; Fig 2H; 154pp; English.
 CC Sequences AAMS2830-AAMS2842 represent novel protein kinase stress-related
 CC proteins (PKSRPs) from the moss Physcomitrella patens, and sequences
 CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
 CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-

CC ABA91068) derived from Physcomitrella patens cDNA libraries. The PKSRPs
 CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7
 CC (PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
 CC homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
 CC homologue-3 (CK-3), mitogen-activated protein kinase (MAP) kinase-2 (MPK-2),
 CC MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
 CC calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
 CC kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
 CC tolerance to environmental stresses such as salinity, drought,
 CC temperature, metal, chemical, pathogenic and oxidative stress.
 CC Physcomitrella patens PKSRP nucleic acids may be used to generate
 CC transgenic plants and seeds with increased tolerance to salinity, drought
 CC and temperature. The transgenic plants generated can be monocots or
 CC dicots and are especially maize, wheat, rye, oat, triticale, rice,
 CC barley, cotton, rapeseed, cassava, sunflower, legumes, leguminous plants
 CC (e.g., soybean, peanut, Vicia species, alfalfa), solanaceous plants
 CC (e.g., potato, tobacco, abubergine, pepper, tomato), coffee, cacao, tea,
 CC Salix species, oil palm, coconut, perennial grasses and forage crops. The
 CC PKSRP nucleotide and proteins may also be used in evolutionary and
 CC protein structural studies and as markers for specific regions of
 CC the genome.
 CC
 XX
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GenCore version 5.1.5
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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 22:21:31 ; Search time 241 Seconds
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Searched: 810007 seqs, 644969091 residues

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and is derived by analysis of the total score distribution.

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1	531.8	30.8	1188	9 US-09-938-842A-644	Sequence 644, App
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3	306.4	17.8	1107	9 US-09-938-842A-1471	Sequence 1471, Ap
C 4	294.4	17.1	953	10 US-09-828-313-8	Sequence 8, Appl
5	233	13.5	1815	9 US-10-072-036-58	Sequence 58, Appl
6	233	13.5	1818	9 US-10-072-036-40	Sequence 40, Appl
7	230.4	13.4	1821	9 US-10-072-036-64	Sequence 64, Appl
8	230.4	13.4	1824	9 US-10-072-036-46	Sequence 46, Appl
9	222.2	12.9	1611	9 US-10-171-311-126	Sequence 126, App
10	212.2	12.3	1308	10 US-09-801-368-149	Sequence 149, App
11	211	12.2	1869	9 US-10-098-841-114	Sequence 114, App
12	211	12.2	1875	9 US-10-072-036-56	Sequence 56, Appl
13	209.6	12.2	1551	9 US-09-938-842A-1067	Sequence 1067, Ap
14	209.4	12.1	1896	9 US-10-072-036-38	Sequence 38, Appl
15	202.8	11.8	1455	10 US-09-801-368-333	Sequence 333, App
16	173	10.0	4280	9 US-10-098-841-283	Sequence 283, App
17	170.2	9.9	1062	10 US-09-801-368-115	Sequence 115, App
18	168.2	9.8	1107	10 US-09-801-368-177	Sequence 177, App
19	168.2	9.8	1838	10 US-09-880-107-1547	Sequence 1547, Ap

20	163.2	9.5	1502	9 US-10-198-343-1	Sequence 1, Appl
21	163.2	9.5	1502	9 US-10-197-315-1	Sequence 1, Appl
22	161.2	9.3	444	10 US-09-770-444-820	Sequence 820, App
23	140.2	8.1	1780	9 US-09-861-097-17	Sequence 17, Appl
24	140.2	8.1	1780	9 US-09-861-098-17	Sequence 17, Appl
25	140.2	8.1	1873	9 US-09-954-531-155	Sequence 155, App
26	135.6	7.9	404	10 US-09-878-574-3791	Sequence 3791, Ap
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28	130.4	7.6	1422	9 US-09-908-650A-23	Sequence 23, Appl
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33	130.4	7.6	2372	9 US-09-165-522-7	Sequence 7, Appl
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41	124.2	7.2	2522	9 US-09-165-522-11	Sequence 11, Appl
42	122.6	7.1	1975	9 US-09-165-522-9	Sequence 9, Appl
43	119.2	6.9	241	10 US-09-878-574-9048	Sequence 9048, Ap
44	116.2	6.7	400	10 US-09-960-352-5288	Sequence 5288, Ap
45	113.8	6.6	773	10 US-09-770-445-905	Sequence 905, App

ALIGNMENTS

RESULT 1

US-09-938-842A-644
Sequence 644, Application US/09938842A
Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joel

APPLICANT: Wang, Xun

APPLICANT: Zhu, Tong

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

FILE REFERENCE: SAME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2000-08-24

PRIOR APPLICATION NUMBER: US 60/264,647

PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 644

LENGTH: 1188

TYPE: DNA

ORGANISM: Arabidopsis thaliana

US-09-938-842A-644

Query Match

Best Local Similarity 69.0%; Pred. No. 1.2e+131; Matches 744; Conservative 0; Mismatches 332; Indels 3; Gaps 1;

QY	157	ATTTCCTCGGTTTAACTACGCGGACATATGATAGTTGATATTTTGGTAAT	216
DB	104	ATTTCCTCGGCTTACCTGAGTGTAGTTATTCAGTAAATATTGGAAACA	163
QY	217	TCTTTGAGATCACTACCAAGATGCTCTCAATATAGCTATGCTGCTGTATG	276
DB	164	TCTTTGAGATCACTACCAAGATGCTCTCAATATAGCTATGCTGCTGTATG	223
QY	277	GAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	336
DB	224	GCATGCTTGTTCGCTATGAAATCTGAAACGAGAGCGCTTGCATTAAGAAATG	283

QY	337	CGAAGGTTGATTAATTAACTGGATGCTTAAGAGGACGTCGCGGTGAATTAACCTCTCC	396
Db	284	CTTAAGCTTTTGACAAATAAGATTGATGCTTAAGAGGACTCTCGGTGAATTAACCTCTTC	343
QY	397	GCCATTTAGACCATGAATAATGTAATTTGGTTAAGAGAGACGTGATTCCTCCACCCTTAAGAA	456
Db	344	GTCAACATGATCATGAAATAATTTGTGCATACAGAGATATTATTCGCCGACCATTTAAGAA	403
QY	457	GGGAGTTTCTGATGTTTACCTTGTCTACTGACACTAGATACTGATCTTTCACCAATAA	516
Db	404	ACGCTTTCAACGATGTTTACCTCCGATGATGATTAATGAAGACACTGATCTTCACCAATAA	463
QY	517	TTAGATCCAAACGAGTTTATCAAGAGATGACGTGCTACTGCTCATGATACAGCTCTCC	576
Db	464	TTGGTCAATACAGCATATTACGAAABAACATTGGCCAGTATTTTCTTTACCAATCTCTC	523
QY	577	GTCGCCTTAAATACATACATTCGCGGATGTTCTTCTATAGAGATCTCAACGAGCAACC	636
Db	524	GTGGATTGAAATATCATCTCACCTGTCAAAATGCTTCCACAGGATTTGAAACCAAGTAATC	583
QY	637	TTTTGGTAAATGCAAAATTTGATTTAAGATATGTGACTTTGGTCCTTGGTAGGCCAAACA	696
Db	584	TTCTCTCTGAACGAAACTGCGACCTAAAAATCTGCGATTTTGGGCTAGCTCGAGTCACTT	643
QY	697	TAGAGAACGAGATATGACGGAATATGTTGTAACAGATGATACAGGCGACCGACGACTTT	756
Db	644	CTGAGAGGATTTTCATCTACTGAAATATGTTGTCCAGAGATGATGACCGTGCACGAGACTTC	703
QY	757	TGTTGAAGCTCTTGAGTTTAACGCTGCTGCTATAGATGTTTGGTCTGTCGCTGGATGCTTCA	816
Db	704	TCTTAAACTCTTCTGATTAATATCTGACACTATTCGATGTTGGTCTGTAAGGCTGATTTTCA	763
QY	817	TGGAAGCTTATGAATAAGAAAACCTTTGTTTGGTGGAAAAAGATCATGTACATCAATAAGCT	876
Db	764	TGGAGTTAATGAGACCGTAAGCACTCTCCCTGGACAGATATCATGTACATCACTTCGCT	823
QY	877	TGTTAACGAGCTCTTGGGCAACCCCAACAGACTGATCTTGGCTTCTCCAAAATGAAG	936
Db	824	TGCTCATGAGACTCATATGGAAGCTCCATCAACAGAAAGGCTCGAGTCTT--GAACGAAA	880
QY	937	ATGCAAGAGATATACATGAGCAATCCCAAGACATCTCCGACAGAGTTAGCAGAGTTT	996
Db	881	ACGCAAAAGCGATACATTAAGAGAGCTTCACCTTATCTCCCAATCATCATGATTAAGT	940
QY	997	TTCCTCATGTGAACCCATTGGCTATTGATCTTGTGCTAAATATGTTGACATTGATCTTA	105
Db	941	TCCCGACAGTCCACTCTTGTAGCTATTAACCTTATCGAAGAGATGTTAAACTTTGATCTTA	100
QY	1057	CTAGAAGATATACAGTTGAGGAACCATTAATCATCTCCCTACCTTGGCAAAAGCTCACGATG	111
Db	1001	GAGCGAGATTCACAGTTTATGAGCGCATTTGGCCACTCATACCTCGAACTGCTTGCACAGCA	106
QY	1117	CAGGTGACGAACCGATCTGCCCTGTTCCATTTCTCTTGACTTTGAGCAACAAGAAATAG	117
Db	1061	TAAACGATGAGCCAGAGTGTACATACCTTTCAACTTTGATTTGAAAAACCATGACACTCT	112
QY	1177	GAGAGAAGCAATTAAGGACATGATATATCAGAAAGCTTTGTACAGTAATCCGATAT	1235
Db	1121	CAGGAGGACATATGAAGCACTAATCTACGCGAGGGGCTTGGTTTCAATTCAGGAATAT	1179

RESULT 2
 US-09-828-313-21
 : Sequence 21, Application US/09828313
 : Patent No. US20020059662A1
 : GENERAL INFORMATION:
 : APPLICANT: COSTA e SILVA, OSWALDO DA
 : APPLICANT: BOHNER, HANS J.
 : APPLICANT: THIELEN, NOCH VAN
 : APPLICANT: CHEN, RODUNG
 : APPLICANT: SARRIA-MILLAN, RODRIGO
 : TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF

	Query Match	Best Local Similarity	24.3%	Score 420:	DB 10:	Length 1718:	
	Matches	654,	Conservative	0,	Mismatches 390,	Indels 0,	Gaps 0,
1	US-09-828-313-21						
2	US-09-828-313-21						
3	US-09-828-313-21						
4	US-09-828-313-21						
5	US-09-828-313-21						
6	US-09-828-313-21						
7	US-09-828-313-21						
8	US-09-828-313-21						
9	US-09-828-313-21						
10	US-09-828-313-21						
11	US-09-828-313-21						
12	US-09-828-313-21						
13	US-09-828-313-21						
14	US-09-828-313-21						
15	US-09-828-313-21						
16	US-09-828-313-21						
17	US-09-828-313-21						
18	US-09-828-313-21						
19	US-09-828-313-21						
20	US-09-828-313-21						
21	US-09-828-313-21						
22	US-09-828-313-21						
23	US-09-828-313-21						
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25	US-09-828-313-21						
26	US-09-828-313-21						
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38	US-09-828-313-21						
39	US-09-828-313-21						
40	US-09-828-313-21						
41	US-09-828-313-21						
42	US-09-828-313-21						
43	US-09-828-313-21						
44	US-09-828-313-21						
45	US-09-828-313-21						
46	US-09-828-313-21						
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67	US-09-828-313-21						
68	US-09-828-313-21						
69	US-09-828-313-21						
70	US-09-828-313-2						

Accession	Sequence	Position
OY	TTCTCATTTATCTGTGCGATATAAATGTTGACATTCGATCCCTACTAGAAAGATTACAGT	1073
OY	1014	
Db	TTCTCTTTATCTTTGTTGAAAAAGATGCGTCTTTGATCCAGCAAAAAGATCACTG	1329
Db	1270	
OY	GAGGAAACATTATGATCATCCCTACCTTGCAGAAAGCTCCAGATGACGATGAGCAAGCCGAT	1133
OY	1074	
Db	GAAAGCTGCTTGGCGCACCCCTTTATTAGCTTCACTTCATGACATCAACGATGAGCCTGCC	1389
Db	1330	
OY	TGCCCTGTTCGATTCCTCTTTCGACTTTGAGCAACAAGATATGAGGAAGCAATTTAAG	1193
OY	1134	
Db	TGCGTATCTCCCTTCGAGTTTGACTTCGAGGAGGCCCCCTATCTCGGAGAGACATATCAAG	1449
Db	1390	
OY	GACATGATATATCAGGAAGCTTTG	1217
OY	1194	
Db	GATCTCAATTTGAGGGAGGCTCTG	1473
Db	1450	

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RESULT 3
US-09-938-842A-1471
: Sequence 1471, Application US/09938842A
: Patent No. US20020160378A1
: GENERAL INFORMATION:
: APPLICANT: Harper, Jeff
: APPLICANT: Kieps, Joel
: APPLICANT: Wang, Xun
: APPLICANT: Zhu, Tong
: TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
: TITLE OF INVENTION: SAME, AND METHODS OF USE
: FILE REFERENCE: SCRIPI300-3
: CURRENT APPLICATION NUMBER: US/09/938,842A
: CURRENT FILING DATE: 2001-08-24
: PRIOR APPLICATION NUMBER: US 60/227,866
: PRIOR FILING DATE: 2000-08-24
: PRIOR APPLICATION NUMBER: US 60/264,647
: PRIOR FILING DATE: 2001-01-16
: PRIOR APPLICATION NUMBER: US 60/300,111
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 5379
: SEQ ID NO 1471
: LENGTH: 1107
: TYPE: DNA
: ORGANISM: Arabidopsis thaliana
US-09-938-842A-1471

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Query Match	17.8%;	Score 306.4;	DB 9;	Length 1107;
Best Local Similarity	58.1%;	Pred. No. 1.7e-71;		
Matches 579;	Conservative	0;	Mismatches 411;	Indels 6; Gaps 2;

[illegible]

QY	576	CGGGCCTTAATACATACATTCGCCGAAATGTTCTTCATAGAGATCTCAACCGACAC	635
Db	430	AAGAGGTGAATATCTTCATCTTCGAAACATCTTCACCGGAGTTTGAAGCCGGGAAC	489
QY	636	CTTTTGGTAAATGCAAAATGTGATCTCTTAAGATATGAGCTTTGGTCTCTAGGCCAAC	695
Db	490	CTCTTAGTTAATGCCAATCGCATCTCAAGATTTTGATTTGGGTTGGCGAAGACGAC	549
QY	696	ATAGAGAACG---AGAAATATGACGGAAATATGTTGTAAACCAGATGGTACAGGSCACCAGAG	752
Db	550	CAAGGTAAATGAACAGTTCATGACTGATGATGTGGTTACACGTTGGTACAGACACTGTAG	609
QY	753	CTTTTGGTAACTCTTCACATTAACAACGTGCTGTATAGATGTTGGTCGTGCGTTGCATC	812
Db	610	CTTCTCTCTTTGTTGTGATATACATATGGAACCTTCATTGATGTAATGGTCGGTTGGTGCATA	669
QY	813	TTTCATGGAATTATGATATGAAACCTTTGTTTGGTGAAGAAATCATGTACATCAATA	872
Db	670	TTCCGGGAATCTCTGGTGTAGGAACCGAATTTTCCAGGAACGAATGCTTGATACAGCTT	729
QY	873	CGCTTGTATACCGAGCTCTTGGCACCCCAACAGAAGCTGATCTTGGCTTCTCCAAAT	932
Db	730	AAGCTATCTATCAACGTTGTTGGTAGCCAAACAAGATCTGATATTCGGTTCTATAGCAAC	789
QY	933	GAGATGCGAAAGATATCATCTCAGGCAACCTCCCAACAATCTCCGACAGATTAGACAGAA	992
Db	790	CCGAAAGCTCGAAGTTTATTAAGTCTCTCCGTACTCAAGAGAACTATCTCTCAAT	849
QY	993	GTTTTCCTCATGTGAACCACTTGGCTATATGATCTTTCGATPAAATGTTGCATTTGAT	1052
Db	850	CTTTATCTCCACAGCCAAATCTCTACTATATAGATTTGTTACAGAGATCGTTGTGTTGAT	909
QY	1053	CCTACTAGAGAATTAACGTTGAGGAAGATTAAGATCAATCCCTACTCTGCAAGCTCCAC	1112
Db	910	CCAAACCAAGAGATCTCTGTAAACGATGGCTCTTACACCCGATATATGGCGGGGTGTTT	969
QY	1113	GATGCAAGTGAACGAACCGATCTGCCCTGTTCATTCTCTCTTGCATTTTGACCAACAAGA	1172
Db	970	GATCTGTGATCCAAATCCGGCTGCACATGHCCCAATCTCTCTGACATATAGATMAAACATG	1029
QY	1173	ATAGAGAAAGCAATTTAAGACATGATATATCAG	1208
Db	1030	GAGGAACCAAGTATTAAGACAGTATGATGGAATGAG	1065

```

RESULT 4
US-09-828-313-8/c
? Sequence 8, Application US/09828313
? Patent No. US20020059662A1
? GENERAL INFORMATION:
? APPLICANT: COSTA e SILVA, OSMALDO DA
? APPLICANT: BOHNETT, HANS J.
? APPLICANT: THIELEN, NOCHA VAN
? APPLICANT: CHEN, ROUYING
? APPLICANT: SARRIA-MILLAN, RODRIGO
? TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
? TITLE OF INVENTION: USE IN PLANTS
? FILE REFERENCE: 16313-0032
? CURRENT APPLICATION NUMBER: US/09/828,313
? CURRENT FILING DATE: 2001-04-06
? PRIOR APPLICATION NUMBER: 60/7196,001
? PRIOR FILING DATE: 2000-04-07
? NUMBER OF SEQ ID NOS: 128
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 8
? LENGTH: 953
? TYPE: DNA
? ORGANISM: Physcomitrella patens
US-09-828-313-8

Query Match          17.1%; Score 294.4; DB 10; Length 953;
Best Local Similarity 62.4%; Pred. No. 2.6e-68;
Matches 477; Conservative 0; Mismatches 286; Indels 1; Gaps 1;

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QY	455	AAGGAGTTTCTTGTGTTTACATGTCTACAGCACTCAGTACTGATGCTTACCAAT	514
Db	931	ACGAGATTTCAACGACGCTGTACATTTGTATACAGATTGATGATGAGCACTTACACAGAT	892
QY	515	AATTAGATCCAAACCAAGGTTTATCAGAGATCCAGTACAGTACTTCATGATACAGCTCT	574
Db	891	CATTCGTTCAATTAACAGCTCTCAGAGAAGACCACTGTGATATTTTGTGTATCAAAATCTT	832
QY	575	CCGTGGCCTAAATATACATACATTTCCGGCAATGTTCTTATAGAGATCTCAACGAGCAA	634
Db	831	GGGGGGCTTGAAGTACATCCATTCGGCGACGCTCTTGACCGGGGACTGAAACCCACCAA	772
QY	635	CTTTTGGTAAATGCAAAATGATGCTTAAGATATGTCACTTGGTCTTGAGGCCAAA	694
Db	771	CTTTCTGCTCAATGCCAATTCGATTTGAAAAATGCCAGATTTTGGCTTGGCACGACTCT	712
QY	695	CATAGAGACGAGAAATATGACGGAATATGTTGTAAACAGATGTTACAGGGCACCGAGCT	754
Db	711	CTCTGAAACGGAATTCATGACTAGTATGTTGTAAAGAGTGTACAGAGCTCCAGAGCT	652
QY	755	TTTGTGAACCTTCAGATTAACCTGCTGCTATATATTTGCTGTGCTGCTGATCTT	814
Db	651	GCTCTGTAATGTTGAGATACACTGACAGCTATTATACATTTGGTCTGTGGGGTGATCTT	592
QY	815	CATGAGACTTATGAATTAACAAAACCTTTGTTGGTGGAAAAAGATCATGTACATCAAAATACG	874
Db	591	CATGAGATTTGCTTAACCGATCTGCTGTGCTGCTGGAGAGACATATGTGATCAGCTCCG	532
QY	875	CTTGTTAACCGAGCTTCTTGGCACCCCAACAGAACTGATCTTGGCTTCTCCAAAATGA	934
Db	531	CCTAATTACAGAACTCATCGGAACCTCGAAGATAGGAGATCTTGGGTTTGTGAGAGGA	472
QY	935	AGATCAAAAGAGATCATCAGGCACTCCACACATCCTCGCCAGCATTTAGAGAAAT	994
Db	471	CAATCTGAGGGGTATATCAAGCACTGCTGCAAGTGCCTATTTCCCTTAACCCAGAA	412
QY	995	TTTCCCTCATGTGAACCCATTTGCTATTGATCTTTCGATAAATATGTTGACATTCAGCT	1054
Db	411	GTTTCAGAGGCAATTAATGCTGTCTGCTGTGATCTTGTGAAAGATGCTGTGTTGATCC	352
QY	1055	TACTGAAAGATTAACGTTGAGGAGAAAGCATTAGATATCCCTACCT-TGCAAAAGCTCCACG	1113
Db	351	AGCGAAAGAAATCAACAGTGGAGAAAGTGCCTTGGCGACCCCTTATTAACTTCACCTTCAATG	292
QY	1114	ATCGAGTGTAGCAACCGAATCTGCTGTTCCATTCCTGCTTGCATCTTGGAGCAACAGAA	1173
Db	291	ACATCAACGATBAGCTGTGCTGGTATCTCCCTTGTGAGTTTGGCTTTCGAGAGGCCCTCTA	232
QY	1174	TAGGAGAGAGCAAAATTAAGGACATGATATATACAGAAAGCTTTG	1217
Db	231	TCTCGAGAGAGCCCTATCAAGGATCTCATTTGGAGAGGAGGCTCTG	188

RESULT 5

US-10-072-036-58

Sequence 58, Application US/10072036

Publication No. US20030082564A1

GENERAL INFORMATION:

APPLICANT: Ole THASTRUP

APPLICANT: Sara BURON

APPLICANT: Soren TULLIN

APPLICANT: Kasper ALMHOLT

APPLICANT: Kurt SCUDDER

TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An

FILE REFERENCE: 3/59-0120P

CURRENT APPLICATION NUMBER: US/10/072,036

CURRENT FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: 09/417,197

PRIOR FILING DATE: 1999-10-07

NUMBER OF SEQ ID NOS: 143

SOFTWARE: PatentIn version 3.0

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: SEQ ID NO 58
: LENGTH: 1815
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Erk2-EGFP fusion
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)..(1812)
US-10-072-036-58

Query Match      13.5%; Score 233; DB 9; Length 1815;
Best Local Similarity 55.2%; Pred. No. 9e-52;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps

OY 258 ATTGTCGTGTGTCCTTATGGAATTTGTCGCTCGGCTCTTCAATACGAGAGCTGAATGATG 317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 85 ATCGGAGAAAGCGCCTACGCGCATGGTTGTCTGCTTATCATATCTCAACAAAGTTGCA 144
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 318 GTTGCAAGTTAAGAAATGCGGATGCGTTGATTTATTTACATGATGCTTAAGAGAGACTCTC 377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 145 GTTGCTATCAAGAAATATC---AGTCCTTTTGGACACACAGACCTACTGTCAGAGAAACCTG 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 378 CGTAGATTAAAGCTCTCTCCGCCATTAGACCATGAAATAGTAATGCTTTAGAGACCGTG 437
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 202 AAGAGATTAAATATCTACTGCGCTTCAGACATGAGAAATCATACGCGCATCAATGATATC 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 438 ATTCTCCACCCCTTACGAAGGAGTTTCTGATGTTTACATGCTCTACTAGCTCATGAT 497
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 262 ATCCGGGACCAACCAACATTGACGAGATGAAAGATGTATATATGTAACAGACCTCATGGAG 321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 498 ACTGATCTTACCAATATATATGATTCACCAACCAAGTTTATCAGAGGATACATGTCAGTAC 557
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 322 AAGAGATCTTTAACAACCTCTTGAAGACACGCA---CCTGAGCAATGATCATATCTGCTAT 378
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 558 TTCAATGATACAGCTCTCCGCTGAGCTAAATATCATATCTCCGCAATGTTCTTCATAGA 617
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 379 TTTCTTTATCAGATCTCTGAGAGGATTTAAAGTATATACATTCAGCTATATGTTCTGCACCGT 438
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 618 GATCTCAAAACGAGCAACCTTTTGGTAAATGCAAAATTTGATCTTAAAGATATGTGACTTT 677
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 439 GACCTCAAGCCCTCCACACTCTCGCTGGAACACACACTTGTGATCTCAAGATCTGTGACTTT 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 678 GGTCTTGC---TAGGCCAAACATAGAGAAGCGAANA-----TGACGGAATATGTT 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 499 GGCCTTGCCTCGGTGACATCCAGACCATGATCATACAGGTTCTTGGACAGAGTATGTA 558
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 726 GTTAACAGATGATGACAGGCGACAGAGCTTTTGTGTAATCTTCACATTAACATCGCTGCT 785
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 559 GCCACGCGTGTGTACAGAGCTCCAGAAATATGTTGAATTCAGAGGTTATACCAAGTCTC 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 786 ATAGATGTTTGGTCTGTGCTGCTGCATCTTCATGGAACCTTATGCAATAGAAAACCTTTGTT 845
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 619 ATTTGATATTTTGGTCTGTGGGCTGATCCCTGGCAGAGATCTATTCCAAAGGCTATCTTCT 678
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 846 GGTGAAAAAGATCATGATACATCAAAATATGACCTTGTATTAACGAGACTTCTTGGACACCCACA 905
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 679 CCAGGAAAGACATTAACCTTGACAGCTGATCATCTCTGGGATTTCTTGGATCTCCATCA 738
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 906 GAAGCTGATCTTGGCTCTCTCCAAAATGAAGATGCAAAAGATATCATCAGGCAACATCCCA 965
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 739 CAGGAAGATCTGAATTTGTTAATTAATTAATAAGCTAAGAAACATATTTGCTTCTCTCCCG 798
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 966 CAACATCTCTCGCAGCAGCTTACAGACAAGTTTTCCTCATGTGAACCCATTTGGCTATGAT 1025
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 799 CACAAAATTAAGGTCCCGTGGAAACAGTTGTTTCCCAAAAGCTGATCCCAAACCTGTGAGT 858
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1026 CTTCGCGATTAATATGTCATTCGCTCTCTACTAGAAAGATATACAGTTGAGGAAGCATTA 1085
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 859 TTACTGATATAATATTGACATTTTAACCTTCACAAAGAGATTGAAGTTTAAACAGGCTCTG 918
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1086 GATCATCCCTACTCTGCAAAAGCTCCACGATGCAAGTACGAACCAATGACCTGCTGTTCCA 1145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


Db 919 GCCCACCCTGACTGAGCAGTATTATGACCCAAAGTGAAGAGCCCATTTGCTGAACACCA 978
Qy 1146 TTCCTCTTGACTTTGACCAACAGAAATAGAGAGAGCAATTAAGACATGATATAT 1205
Db 979 TTCAGTTTGACATGAGCTGAGCAGCTTACCTTAAGAGAGAAAGCACTCAATTTT 1038
Qy 1206 CAGAAAGCTTTGCTCAGTAATCTGTAATA 1234
Db 1039 GAAGAGACTGCTCGATTCAGCAGCAGGATA 1067

RESULT 6
US-10-072-036-40
: Sequence 40, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 40
: LENGTH: 1818
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: EGFP-Erk2 fusion
: NAME/KEY: CDS
: LOCATION: (1)..(1815)
US-10-072-036-40

Query Match 13.5%; Score 233; DB 9; Length 1818;
Best Local Similarity 55.2%; Pred. No. 9.1e-52;
Matches 546; Conservative 0; Mismatches 425; Indels 18; Gaps 4;

Qy 258 ATTGCTGCTGCTTATGGAATTTCTCTGCTGGTGTGATACGAGAGCTGAATGATG 317
Db 826 ATCGGAGAAGGCGCTACGGATGGTTGTTCTGCTTATGATTAATCTCAACAAAGTTGCA 885
Qy 318 GTTGACGTTAGAAAATGCGAATCGTTTGTATTTACATGATGCTAAGAGAGCTGC 377
Db 886 GTTGATCAAGAAAATC---AGTCTTTTGAAGCACCAGAGCTACTGTCAAGAAACCTTG 942
Qy 378 CGTGAATTAAGCTCTCCGCAATTTAGACATGAATAATGATTGTTTAAAGACGTG 437
Db 943 AGAGAGATAAAATCTCACTGCGCTTCAGACATGAGAACATCATCGGATCAATGACATC 1002
Qy 438 ATTCTCACCCTTACGAAGGAGTTTCTGATGTTTACATTTGCTACTGCAATCTGAT 497
Db 1003 ATCGGGAGCCAAACCATTTGAGAGATGAAGATGATATATAGTACAGAGACTCATGAG 1062
Qy 498 ACTGATCTTCAACAAATATTAATGATCAACCAAGGTTTATCAGAGATCATGTCAGTAC 557
Db 1063 ACAGATCTTTCAAGCTCTTGAAGACACAGCA---CTCAGCAATGATCATATCTGCTAT 1119
Qy 558 TTTCATGATCAGCTCTCGTGGCCCTAAATACATATTCGCGAATGTTCTCATAGA 617
Db 1120 TTTCTTTATCAGATCTCTGAGGATTAAGATATATACATTCAGTAAAGTCTGACCGT 1179
Qy 618 GATGCAAAAGCAGCAACTTTTGTGAATGCAATGCTGAATCTTAAGATATGACTTT 677
Db 1180 GACCTCAAGCTTCCAACTCTGCTGTAACACCACTTGTGATCTCAAGATCTGTGACTTT 1239

Qy 678 GGTCTTGC---TAGCCAAACATAGAGAAGAGATA-----TGACGAATATGTT 725
Db 1240 GGCCTTGCCCGTGTGTCAGATCCAGACATGATATCATACAGGCTTCTTGACAGATATGA 1299
Qy 726 GTAACAGATGGTACAGGGCACCAGAGCTTTTGTGAACCTCTTCAGATATACACTGCTGT 785
Db 1300 GCCACGCGTTGGTACAGAGCTCCAGAAATTAATGTAATTCAGAGGTTATACCAAGTCC 1359
Qy 786 ATGATGTTTGGTCTGTGCTGTTGATCTTCATGAGAACTTATCAATAGAAAACCTTGTT 845
Db 1360 ATTGATATTGTTGCTGTGGGCTGATCTCGCAGAGATGCTATCCAGAGGCTATCTTC 1419
Qy 846 GGTGAAAAGATCATGTACATCAATACGCTGTTTAACCGAGCTTCTTGACCCACCA 905
Db 1420 CCAGAAAGCAATTTACCTTGACCAAGCTGAATCATCTCTGGATTTCTTGATCTCCATCA 1479
Qy 906 GAAGCTGATCTTGGCTCTCCCAAAATGAAGATGCAAGATACATCAGGCAACTCCCA 965
Db 1480 CAGGAAGATCTGAATGATTAATTAATTAAGCTAGAAACTATTTGCTTCTCCCG 1539
Qy 966 CAACATCTCGCCAGCAGTTAGCAGAGTTTCCCTCATGTGAACCATTTGCTATTGAT 1025
Db 1540 CACAAAATTAAGTCCCGTGGAACAGTTGTCCCAACGCTGACTCCAAAGCTCTGGAT 1599
Qy 1026 CTGTGCGATAAATGTTGACATTTGATCCTACTAGAGAATTAACAGTTGAGAGAGCATTA 1085
Db 1600 TTACTGATTAATGTTGACATTTTAACCTTCACAAAGAGATTTGAATGAACAGCTCTG 1659
Qy 1086 GATCATCCCTACCTTGCAAAAGCTCCACATGAGGTGACGAACGATGCTCCCTTGCA 1145
Db 1660 GCCCACCCTGACTGAGAGAGATTAATGACCCAAAGTATGAGCCCATTTCTGAACACCA 1719
Qy 1146 TTCCTCTTGACTTTGAGCAACAAAGAAATAGAGAAAGCAATTAAGACATGATATAT 1205
Db 1720 TTCAAGTTTGACATGAGCTGAGCAGCTTACCTTAAGAGAAAGCTCAAAAGACTCATTTT 1779
Qy 1206 CAGAAAGCTTGTCACTGAATCTGTAATA 1234
Db 1780 GAAGAGACTGCTCGATTCAGCAGCAGGATA 1808

RESULT 7
US-10-072-036-64
: Sequence 64, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
: FILE REFERENCE: 3759-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: CURRENT FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 64
: LENGTH: 1821
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: p38-EGFP fusion
: NAME/KEY: CDS
: LOCATION: (1)..(1818)
US-10-072-036-64
Query Match 13.4%; Score 230.4; DB 9; Length 1821;
Best Local Similarity 56.4%; Pred. No. 4.5e-51;

Matches	495	Conservative	0	Mismatches	371	Indels	12	Gaps
OY	255	CCTATTGGTCGGTGGCTTTATGGAATTTGCTCTCGTGGTTGGAATTCGAGCTGAATGAG	314					
Db	85	CCAGTGGGCTCGGGCCCTATGGCTCTGTGTGTGCTCTTTTGACCAAAAACGGGGTTA	144					
OY	315	ATGTTTGACGATTAGAAATAATCGCAATGGCTTTGATATTACATGATGCTCTAAGAGACT	374					
Db	145	CGTGTGGCAGTGAAGAAGCTCTCCAGACATTTCAGTCCATCATCTATCTCGAAAAAGAAC	204					
OY	375	CTCCGTGAGATTAAAGTCTCTCCGCCATTTAGACCATGAAATGTAATTGGTTTAAAGAAC	434					
OY	435	GGATT --- CCHCACCCCTTAGCAAGGCGTTTTCGATGTTTAACTGCTCTGACAC	491					
Db	265	GTTTTTACACCTGCGAAGGTCTCTGGAGGAAATTCATGATGTGTATCTGTGTGACCATCTC	324					
OY	492	ATGATACTGATCTTCCACCAATAATTAGATCCAAACCAAGTTTATCAGAGATCACTGT	551					
Db	325	ATGGGGGCGAGATCTGMAACAATTTGGAAAT --- GTCAGAAGCTTACAGATGCCATGTT	381					
OY	552	CAGTACTTCATATACAGTCTCTCCGTGGCTTAAAAATACATACATTCCCGCAATGTCTT	611					
Db	382	CAGTCTCTTATCTACCAAAATTTCTCCGAGGTCTAAAGTATATACATTCACTGACATAATT	441					
OY	612	CATTAAGATCTCTAAACCCGACAACTTTTGTGTAATCTGTAATTTGATTTAAATATGT	671					
Db	442	CACAGGAGACTAAACCTAGTATATGATGATGATGATGATGATGATGATGATGATGATGAT	501					
OY	672	GACTTTGGTCTTTGCTAGGCCAAACATAGAAACGAGATATGACGAAATGTGTTAAC	731					
Db	502	GATTTTGGACTGCTGGCGGACA ----- CAGATGATGAATATGACAGGCTACGCGCACT	555					
OY	732	AATGTGACAGGAGCACACAGCTTTTGTGTAACCTCTTGATTAACCTCTGCTATATGAT	791					
Db	556	AGGTGTACAGGGCTCTCTAGATCATGCTGAACCTGGATGATCATACACAGACGTTGAT	615					
OY	792	GTTTGGCTGTCGGTTGCACTTTCATGGAACCTTATGATAAATAAAACCTTTGTTGGTGA	851					
Db	616	ATTTGGTCACTGGGAGTCAATATGCGCGAGCTGTTGACGTAAGAAACATTTGCTCTGCT	675					
OY	852	AAAGATCATGTCAATCAATATAGCTTTGTAACCGAGCTCTTGGACCCCAACAGAGAGT	911					
Db	676	ACAGACCATATGATCATGTTGAAGCTCATTTTAAAGCTCTGTTGAACCCACAGGGCTGAG	735					
OY	912	GATCTTGGCTCTCCCAAAATGAAAGATGCAAGAGATATACATAGGCAATCCCAACAT	971					
Db	736	CTTTGAAGAAATCTCTCAGAGTCTCCAGAAACTATATATCAAGTCTTGAAGCTGAG	795					
OY	972	CCTCGCAGCATTTAGCAAGAATTTTCCCTCATGTGAACCATTTGGCTATTGATCTTGTC	1031					
Db	796	CCGAAGATGAACCTTTCGAAATGATTTATTTATTTGTCGCAAACTCCCTGCTGCACTTGCG	855					
OY	1032	GATTAATTTGATCATCTCATCTAGAAATAATTACAGTTGAGAGACATTATGATCAT	1091					
Db	856	GAGAGATGCTGTATGTGACTCAGATATAGAGATTTACAGCGGCCCAACCTTGCACAT	915					
OY	1092	CCCTACCTTGCAAAAGCTCCAGATGACAGGTGACGAAC	1129					
Db	916	GCTTACTTTGCTCAGTACCAAGCATCTGTATGATGAAC	953					

[illegible]

Db 1537 CGAAGATGAACCTTGGCGAATGATATTAATGTTGCCAATCCCTGGCTGACACTTGC 1596
Qy 1032 GATAAATGTTGACATTTGATCTCTACTAGAGAATTTACAGTTGAGAGCAATTAGATCAT 1091
Db 1597 GAGAAGATGCTTGTATTTGACACAGATTAAGAATTTACAGCGCCCAACCCCTTGACAT 1656
Qy 1092 CCGTACTTGCATCCAGATGACGAGTGAGCAACC 1129
Db 1657 GCCTACTTGTCTCAGTACGACGATCCTGATGATGAACC 1694

RESULT 9

US-10-171-311-126
: Sequence 126, Application US/10171311
: Publication No. US20030087270A1
: GENERAL INFORMATION:
: APPLICANT: Schlegel, Robert
: APPLICANT: Chen, Yan
: APPLICANT: Zhao, Xumei
: APPLICANT: Monahan, John
: APPLICANT: Kamatkar, Shubhangi
: APPLICANT: Gialt, Karen
: APPLICANT: Gannavairapu, Manjula
: APPLICANT: Hoerish, Sebastian
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
: TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
: TITLE OF INVENTION: OF CERVICAL CANCER
: FILE REFERENCE: MRI-035
: CURRENT APPLICATION NUMBER: US/10/171,311
: CURRENT FILING DATE: 2002-06-12
: PRIOR APPLICATION NUMBER: US 60/298,159
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/298,155
: PRIOR FILING DATE: 2001-06-13
: PRIOR APPLICATION NUMBER: US 60/335,936
: PRIOR FILING DATE: 2001-11-14
: NUMBER OF SEQ ID NOS: 238
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 126
: LENGTH: 1611
: TYPE: DNA
: ORGANISM: Homo sapiens
US-10-171-311-126

Query Match 12.9%; Score 222.2; DB 9; Length 1611;
Best Local Similarity 53.9%; Pred. No. 6.5e-49;
Matches 533; Conservative 0; Mismatches 438; Indels 18; Gaps 3;

Qy 258 ATTGCTCGTGTCTTATGGAATTCCTGCTGCTGTTGAATACGAGCTGAATGATG 317
Db 418 ATCGCGAGGGGGCTAGCGATGCTGCTGCTTATGATTAATGTCACAAAGTTGCA 477
Qy 318 GTTGAGTTAAGAAATGCGCAATGCGTTTGAATTTACAGTGAATGAGGAGCACTCTC 377
Db 478 TAGCTATCAAGAAATC---AGCCCTTTGAGCACACGACCTACTGCCAGAACCCG 534
Qy 378 CGTGAGATTAAAGCTCCCGCCATTAGACCATGAATAATGTAATGGTTTAGAACG 437
Db 535 AGGGAGATAAAATCTTCTGCGCTTCAGACATGAGAACATCATTTGGAATACAT 594
Qy 438 ATTCTCCACCTTACGAAGAGATTTTCTGATGTTTACATTTGTAAGTCACTGATGAT 497
Db 595 ATTGAGACACCAACCATGAGCAATGAAGATGATATATATGTAAGAGCACTCATG 654
Qy 498 ACTGATCTTACCAATATTAATGATCAACCAAGGTTTATACAGAGATCACTGTGAC 557
Db 655 ACAGATCTTTACAGCTCTTGAAGACACACCTCAGCAATACCATATCTG---CTAT 711
Qy 558 TTCATGATCAAGCTCCCGGCGCTTAATATACATATCCGCAATGTTTCTTACAGA 617
Db 712 TTCTCTACAGATCTCAGAGGGTTAAATAATATATACATGATGATGATGACCGT 771

Qy 618 GATTCAAACGACGACACCTTTGGTAATGCAAAATGATGCTTAAATATGATGACTTT 677
Db 772 GACCTTCAGCCTTCCACCTGCTGCTCAACACACCACTGATATCTCAAGTCTGTGACTTT 831
Qy 678 GGTCTTGC-----TAGGCCAAACATAGAGAACGAGAAATATGACGGAATATGTT 725
Db 832 GGCTGCGCCCGTGTGACATCCAGACATGATGATCAGACAGGGTCTCCTGACAGAAATATG 891
Qy 726 GTAACCATGATGATACAGGCGACAGCTTTGTTGAATCTTTCAGATTTACATGCTGCT 785
Db 892 GCCACACGTTGGTACAGGGCTCCAGAAATTAATGTAATTCAGAGGCTCAGACCAATGCC 951
Qy 786 ATAGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 845
Db 952 ATTGATATTTGGTCTGTAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Qy 846 GGTGAAAAGATCATGTACATCAATAGCCTTGTAAACGAGCTTTTGGACCCCA 905
Db 1012 CCAGGAAGCATTAATCTTACAGCAGTGAATCAATTTGGTATTTCTGATCCCATCA 1071
Qy 906 GAAGCTGATCTTGGCTCTCTCCAAAATGAAGATGCAAGAGATACATCAGCACTGCCA 965
Db 1072 CAAGAAGACCTGAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1131
Qy 966 CAACATCTCGCCAGCAGTACAGAGATTTCCCTCATGTAAACCATTTGGCTATTTGAT 1025
Db 1132 CACAAAATTAAGTGCATGAGAACAGGCTGTTCCCAATGCTGATCCCAAGCTGGAC 1191
Qy 1026 CTGTGATTAATTAATGTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 1085
Db 1192 TTATTGACAAATATGTTGACATTTCAACCAACAGAGATGAGTGAACAGGCTG 1251
Qy 1086 GATCATCCCTACTTGCAGAACGCTCCAGATGAGTGAAGAGAACCATCTGCTGTCCA 1145
Db 1252 GCCACCCATATCTGAGCAGATTAACGACCGAGTGAAGAGACCATCCCAAGACCA 1311
Qy 1146 TTCTCCTTGTGACTTGAAGCAAGCAATAGAGAAATTAAGCAATTAAGCAATTAAT 1205
Db 1312 TTCAGTTGACATGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1371
Qy 1206 CAGGAAGCTTTGCTCACTGATCTCTGATA 1234
Db 1372 GAAGAGACTGTAGATTTCCAGCCAGGATA 1400

RESULT 10

US-09-801-368-149
: Sequence 149, Application US/09801368
: Patent No. US20020128250A1
: GENERAL INFORMATION:
: APPLICANT: Busby, Robert
: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin
: APPLICANT: Maxon, Mary
: APPLICANT: Milne, Todd
: APPLICANT: No. US20020128250A1man, Thea
: APPLICANT: Royer, John
: APPLICANT: Salama, Sofie
: APPLICANT: Sherman, Amir
: APPLICANT: Silva, Jeff
: APPLICANT: Summers, Eric
: TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
: FILE REFERENCE: 109272.147
: CURRENT APPLICATION NUMBER: US/09/801,368
: PRIOR FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 09/487,558
: PRIOR FILING DATE: 2000-01-19
: PRIOR APPLICATION NUMBER: US 60/160,587
: PRIOR FILING DATE: 1999-10-20
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: PatentIn version 3.0

QY	1206	CAGGA	1210
Db	1099	CAGGA	1103

```

US-09-938-842A-1067
RESULT 13
US-09-938-842A-1067
Sequence 1067, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kieps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIPT300-3
CURRENT APPLICATION NUMBER: US/09/938, 842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264, 647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300, 111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1067
LENGTH: 1551
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1067
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Query Match	12.2%;	Score 209.6;	DB 9;	Length 1551;
Best Local Similarity	53.5%;	Pred. No. 1.5e-45;		
Matches 493; Conservative	0;	Mismatches 414;	Indels 15;	Gaps 2

Oy	257	TAAAGTCGTGGTGGTAAATGGAATGTCCTCGTGGTTGAATTCGGAAGCTGAATGAT	316
Db	63	TGTTGGCAAAAGGAGCTACGGAGGTGTTGCTTTCGCGGAATGTCACACAGGGAGCAA	122
Oy	317	GGTTGCACCTTAAGAAAATCCGGAATGCGTTGATATTACATGATGCTTAAGAGACTCT	376
Db	123	AGTACCCATCAAGAAAGATGACAATATGTTGTTGAACATGTCACAGATCTATTCGTATCCT	162
Oy	377	CCGTGAGATTAACTCCTCCGCCATTAGACCAATGAATGTAATGTTAGTTAAGAGAGCT	436
Db	183	CAGAGAGATCAAGCTTCTCAGGCTTCTTCGACATCTGATATCGTGAGATCAAGCATAT	242
Oy	437	GATTCCTCCACCCTTACGAAAGGAGCTTTCTGATGTTTACATTGCTACTGAACATGGA	496
Db	243	CATGCTTCTCCTCTTGTCGCAAGGAATTCMAAGATATATATGTTGTTTGTTAGTTGGA	302
Oy	497	TACTGATCTTCACCAAAATTAATTAGATCCAACCAAGGTTTATCAGAGATCACTGTCGTA	556
Db	303	GTCGTATCTTACCAACGTTCTTAAAGTCAAAATGACGACTCACTCTTAGCATCATATT	362
Oy	557	CTTCATGATCAGTCTCCGCTGGGCTAAATATACATACATCCGCGAATGTTCTTCTATAG	616
Db	363	CTTCTTGACCAACGTTCTTGCGCTTAAATTCATGCACACACCTCATGTGCCATAG	422
Oy	617	AGATCTCAACCGAGCAACCTTTTGGTAAATGCAAAATTGCATCTTAAGATATGTACTT	676
Db	423	AGATCTGAAGCTCAAGAACATCTCGCTAAATGCTGATGCAAAATCAAGATCTGATTT	482
Oy	677	TGCTTCTCTAGGCCAAACATAGAGAA-----CGAGAAATGACGGAATATGT	724
Db	483	AGGAACTCTCGTGTCTTCCTTACTGATTCCTCCCTTCGCTGTGTTTGGAGTCACTACGT	542
Oy	725	TGTAAACGAGTGGTACAGGAGCAGAGACT---TTGTGTGAACCTCTCAGATTACACTGC	781
Db	543	TGCTAACAGATGGTACGTGGCGCCAGAGACTTGTTGTTCCCTTATTTCTACTACAGGC	602

Oy	782	TGATATGATGTTGGTCCTGGTTGGATCCTTCATGAGAACTATGAAATAGAAACCTT	841
Db	603	GGCCATTGCATGTGGAGATGTGGGTGCATATTTGCAGAGATGCTACTGAGAAACCTTT	662
Oy	842	GTTTGTGGAGAAAGATCATGTATACATCAAAATACGCTGTTAACGAGACTCTTGGCACCC	901
Db	663	GTTTCTCTGGCAAAACGTTGTGCACCAAGCTAGAAAGCTGTGATGATCTGTGGAATCC	722
Oy	902	AACGAAAGCTGATCTTGGCTTCCCTCCAAATGAAAGATGCAAAGACATATCAGGCACCT	961
Db	723	GTCGCCGATTAACCTATATCCAGGATTCGGATGAGGAAGGTACAAAGTATTTGGGAAACAT	782
Oy	962	CCCACAAATCTCTGGCCAGCAGTAGAGAGAAGTTTCCCTCAGTATGAAACCAATTTGGCTAT	1021
Db	783	GAGGCGAAAGGATCTGTACCTTTCACCCCTAAATTTCCCAATATCGATCTGTGGCGT	842
Oy	1022	TGATCTTGTGCATAAATGTTGACATTCGATCCCTACTAGAGAAATATACAGTTGAGAGAAGC	1081
Db	843	GAACTTACTTCAGGGTTTGATCCGCTTTTGGACCCAAAGAGACGTCCTCTGCAGAAAGAGCG	902
Oy	1082	ATTAGATCATCCCTTACCTTCGAAAGCTCCACGATGCAGGTGACGAACGATCGCCTGT	1141
Db	903	ATTGGCTGATCCGTAATTTTCAGAGATTCGCAATGTGCACTATGACCAATCAGAGCAACC	962
Oy	1142	TCCATTTCTCCTTGACTTTGAG	1163
Db	963	TATCTCGAAACTTGAGTTGAG	984

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RESULT 14
US-10-072-036-38
; Sequence 38, Application US/10072036
; Publication No. US20030082564A1
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP
APPLICANT: Sara BJORN
APPLICANT: Soren TULLIN
APPLICANT: Kasper ALMHOLT
APPLICANT: Kurt SCUDDER
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0120P
CURRENT APPLICATION NUMBER: US/10/072.036
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/417,197
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 38
LENGTH: 1896
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EGFP-Erk1 fusion construct
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1893)
US-10-072-036-38

```

Query Match	12.1%;	Score 209.4;	DB 9;	Length 1896;
Best Local Similarity	53.5%;	Pred. No. 1.9e-45;		
Matches 516;	Conservative 0;	Mismatches 431;	Indels 18;	Gaps 37;

QY 258 ATGTGCTGGTGGTTATGGAATGTCTGCTCGGTGTGAATATGCGAGCTGAATGAATG 317
Db 888 ATCGCGAGGCGCGCTACGGCATGTCTACCTCGGCTATGACCGTGGCCAGACTCCG 957
QY 318 GTTCGAGTTAAGAAATCGCAATGCGTTGATATTACATGATGCTAAGAGAGACTTC 3777
Db 958 GTGGCGATCAAGAAGATC -- AGCCCTGTGACATCAGACCTACTCCAGCGGACGCTC 101
QY 378 CGTGAGATTAGCTCTCCGCCATTAGACCATGATAAATGTAAATTGGTTTAAGAGACGTG 437


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Db      789  AAATGTTACAGACTACATCATCATTAATGAGTTTCATTCCAAAGTACCTTTGTCATTT 848
QY      995  TTCCCTCATGTGAAGCCATTGGCTATTTGATCTTGCGATATAAATGTTGACATTGATCC 1054
Db      849  ATACCCAAATGCCAATTCAAGCATTTAGACTTATTTGAGCAAAATGCTCGCGTTTGACCC 908
QY      1055 TACTAGAGATTTACAGTTGAGAGCATTCATCCCTTACCTTGCAAGCTCCACGA 1114
Db      909  TCAAAAGAGATTTACCGTGTGATGAGGCCCTGAGCATCTTACTTGCTATATGCGATGA 968
QY      1115 TCGAGGTGACGAACCGATCTGCCCTGTTCCATTCCTCTTGAAGTTGA 1162
Db      969  TCCAGCTGACGAACCTGTGTGTAGTGAATAATTCGAATTTAGTTTGA 1016
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Search completed: May 20, 2003, 00:20:30
Job time : 259 secs

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OM nucleic - nucleic search, using sw model

Run on: May 19, 2003, 20:56:06 ; Search time 2257 Seconds
(without alignments)
12378.030 Million cell updates/sec

Title: US-09-623-034-1
Perfect score: 1725
Sequence: 1 tatataaccatagctca.....gagcaagagactggtgata 1725

Scoring table: IDENTITY:NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:
1: em_estba:*
2: em_esthu:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
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15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
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20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	637.6	37.0	735	13	BM409226 EST583553
2	598.8	34.7	702	13	B1922618 EST542522
3	545.6	31.6	850	14	B0164817 EST610686
4	545.4	31.6	1715	11	AT108471 Zee mays
5	541.8	31.4	609	9	AT488693 EST247032
6	517	30.0	629	10	AW038184 EST279841

	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45																																																																																																																																																							
LOCUS	503.4	29.2	603	14	B0507523	503.4	29.2	605	12	BG597996	481.8	27.9	605	10	AM979631	471	27.3	1705	11	AT105588	465.6	27.0	712	10	AM776266	452.6	26.2	507	10	AM034815	450.6	26.1	699	10	AM775836	449	26.0	679	10	AM775829	447.2	25.9	672	10	AM684379	436.8	25.3	758	14	AM775798	429.2	24.9	635	14	B0851303	427.8	24.8	742	12	BG582359	413.4	24.0	685	10	AM773944	409.2	23.7	494	10	BE459015	406.2	23.5	713	10	BE662883	401.8	23.3	592	12	BF520309	392	22.7	687	12	BF644893	391.6	22.7	679	9	AT781537	389.6	22.6	597	12	BG042780	389.6	22.6	650	10	AM775768	388.6	22.6	702	10	AM256695	385	22.3	594	14	B0629175	384.6	22.3	666	12	BF648477	383.2	22.2	613	10	AM459389	383	22.2	596	14	B0079600	380.6	22.1	638	14	BF005291	377	21.9	685	12	B0028085	377	21.9	713	14	B0116156	373.8	21.7	863	10	BE412950	373	21.6	794	14	B0164988	371.4	21.5	590	10	BE123964	371.4	21.5	643	12	BE647281	369.4	21.4	570	13	BM527070	369.4	21.4	693	12	BF634735	366.2	21.2	625	12	BG580947	366.2	21.1	560	9	AT487449	362.2	21.0	630	12	BF645965	362.2	21.0	567	13	B1892783

ALIGNMENTS

RESULT 1
LOCUS BM409226 735 bp mRNA linear EST 22-JAN-2002
DEFINITION EST583553 tomato breaker fruit Lycopersicon esculentum cDNA clone
ACCESSION CLEG47N15 5' end, mRNA sequence.
VERSION BM409226
KEYWORDS BM409226.1 GI:18260856
SOURCE EST.
ORGANISM tomato.
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
REFERENCE 1 (bases 1 to 735)
Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai
,J., Bougri,O., Kirchner,E., Uterback,T., Van Aken,S., Roming
,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
Generation of ESTs from tomato fruit tissue, breaker stage (2002)
Unpublished (2002)
CONTACT CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
Location/Qualifiers

```

source
1. .735
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato breaker fruit"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/note="Vector: pBluescriptSkmUnidapt; Site.1: EcoRI;
Site.2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."

BASE COUNT      218 a      149 c      151 g      217 t
ORIGIN
Query Match      37.0%; Score 637.6; DB 13; Length 735;
Best Local Similarity 92.5%; Pred. No. 3.6e-124;
Matches 681; Conservative 0; Mismatches 54; Indels 1; Gaps 1;

QY 301 CGGAGCTGATGAGATGGTTCAGTTAAGAAATCGCGAATGCGTTGATTTACATGG 360
Db 1 CGGAGCTGAATGAGATGGTTCAGTTAAGAAATCGCGAATGCGTTGATTTACATGG 60
QY 361 ATGCTAAGAGACCTCCGAGATTAAGCTCCGCCATTTAGACCATGAATAATGTA 420
Db 61 ATGCTAAGAGACCTCCGAGATTAAGCTTCCTCCCATTTAGACCATGAATAATGTA 120
QY 421 TTGGTTTAAGAGACGATTCCTCCACCTTACGAAGGAGTTTGTGATGTTTACATG 480
Db 121 TTGGTTTAAGAGATGATTCCTCCGCCCTTACGAAGGAGTTTGTGATGTTTACATG 180
QY 481 CTACTGAACATGAGATGATGATTCCTCCGCCATTTAGACCATGAATAATGTA 540
Db 181 CTACTGAACATGAGATGATGATTCCTCCGCCATTTAGACCATGAATAATGTA 240
QY 541 AGGATCTGCTCAGTACTTATGATGAGCTCCCGGCTTAATATACATTCATTCG 600
Db 241 AGGATCTGCTCAGTACTTATGATGAGCTTCGCCGCTTAATATACATTCATTCG 300
QY 601 CGAATGCTTTCATAGAGATCTCAACCGAACAACCTTTGGTAATGCAAAATGTGATC 660
Db 301 CGAATGCTTTCATAGAGATCTCAACCGAACAACCTTCCTTAATGCAAAATGTGATC 360
QY 661 TTAGATATGATGCTGGCTGCTGCTAGGCCAATAGGAAGGAATATGCGAAT 720
Db 361 TTAGATATGATGCTGGCTGCTGCTAGGCCAATAGGAAGGAATATGCGAAT 420
QY 721 ATGTTGTACAGATGCTAGAGGCGACAGAGCTTTGTTGAACCTCTTCAGATTACAG 780
Db 421 ATGTTGTACAGATGCTAGAGGCGACAGAGCTTTGTTGAACCTCTTCAGATTACAG 480
QY 781 CTGCTATATGATGTTGGTCTGTGGTGATCTTCATGGAACCTTATGAATGAACCTT 840
Db 481 CTGCTATATGATGTTGGTCTGTGGTGATCTTCATGGAACCTTATGAATGAACCTT 540
QY 841 TGTGTTGGTGAAGAAATGATGATGATCAATAGCTTGTATACCGAGCTCTTGGCACC 900
Db 541 TGTGTTGGTGAAGAAATGATGATGATCAATAGCTTGTATACCGAGCTCTTGGCACC 600
QY 901 CAACAGAAAGTGAATCTGGCTCCCAATGAAATGAAAGATGAAATGATATGAGGAG 960
Db 601 CTACAGAAATGATGATCTGCTCCGTAATGAAATGAAAGATGAAATGATGAGGAG 660
QY 961 TCCACAAACATCTCGCCAGCAGTTAGCAGAAATTTCCCTCATGTAGCAACCATTTGCTA 1020
Db 661 TCCACAAACATCTCGCCAGCAGTTAGCAGAAATTTCCCTCATGTAGCAACCATTTGCTA 719
QY 1021 TTGATCTTGTGATTA 1036

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Db 720 TTGATCTGTGATTA 735

RESULT 2
BI922618
LOCUS
DEFINITION
EST542522 tomato callus Lycopersicon esculentum cDNA clone cLEC78E9
5' end, mRNA sequence.
ACCESSION
BI922618
VERSION
BI922618.1 GI:16220423
KEYWORDS
EST.
SOURCE
tomato.
ORGANISM
Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 702)
Alcala, V., Vredalov, J., White, R., Vision, T., Karamycheva, S.A., Tsai
, J., Utecherback, T., Van Aken, S., Roming, C.M., Fraser, C.M., Martin
, G.B., Tanksley, S.D. and Giovannoni, J.
Generation of ESTs from tomato callus tissue (2001)
Unpublished (2001)
CONTACT: CUGI
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
Seq primer: T3.
FEATURES
Location/Qualifiers
1..702
/organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone_lib="tomato callus"
/tissue_type="callus"
/dev_stage="25-40 days old"
/lab_host="XJ1-Blue MRF"
/note="Vector: pBluescript SK(-); Site.1: EcoRI; Site.2:
XhoI; supplier: Boyce Thompson Institute; sequencing: The
Institute for Genomic Research; cLEC - Cotyledons of
seedlings 7-10 days post-germination were excised, cut at
both ends and placed on MS medium with no selection. Mixed
callus was harvested at 25 and 40 days and included
undifferentiated masses. Tomato Callus EST Library"

BASE COUNT      198 a      132 c      148 g      224 t
ORIGIN
Query Match      34.7%; Score 598.8; DB 13; Length 702;
Best Local Similarity 91.1%; Pred. No. 5.3e-116;
Matches 636; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 138 GGTGAGGTCATATCCCTGATTTCTCGGTTTAACTACGCGGAGCAATATGACAG 197
Db 5 GGTGAGGTCATATCCCTGATTTCTCGGTTTAACTACGCGGAGCAATATGACAG 64
QY 198 TTTGATATTTTGGTATTTCTTGGATGATGATGATGATGATGATGATGATGATGAT 257
Db 65 TATGACATTTTGGTATTTCTTGGATGATGATGATGATGATGATGATGATGATGAT 124
QY 258 ATTGAGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 317
Db 125 ATTGAGCTGTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 184
QY 318 GTTGCACTTAAGAAATCGGAAATCGTTGATATTTACATGATGATGATGATGATGAT 377
Db 185 GTTGCACTTAAGAAATCGGAAATCGTTGATATTTACATGATGATGATGATGATGAT 244
QY 378 CGTGAGATTAAGCTCTCGCCCATTTAGACCATGAATAATGTTATGTTAAGAGACG 437

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FEATURES	source
RESULT 3	
LOCUS	
BO164817	
DEFINITION	BO164817 850 bp mRNA linear EST 25-APR-2002
ACCESSION	EST610686 KYKC Medicago truncatula cDNA clone pKYC-1G8, mRNA
VERSION	sequence.
KEYWORDS	BO164817
SOURCE	BO164817.1 GI:20306222
ORGANISM	EST.
	barrel medic.
	Medicago truncatula
	Eukaryotes: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
	Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
	Rosidae: eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
	Medicago.
REFERENCE	1 (bases 1 to 850)
AUTHORS	Vandenbosch,K., Endre,G., Silverstein,K., Town,C.D., Van Aken,S.,
TITLE	Uterback,T., Cheung,F. and Fraser,C.M.
JOURNAL	The Medicago truncatula 'Kilcloone' set: ESTs selected and
COMMENT	re-arrayed from various libraries
	Unpublished (2002)
	Contact: Vandenbosch K
	Department of Plant Biology
	University of Minnesota
	220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
	Tel: 612 624 2755
	Fax: 612 625 1738
	Email: kvandenbosch.umn.edu
	TIGR sequence name: MTRNA807B Alias Clone name: KV0-1J2 More
	Information is available at: www.medicago.org
	Seq primer: Skmod (CTA gaa CTA gtg gat CC).
	location/Qualifiers
	1..850

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the UniZap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL10R cells."

Query Match	31.6%	Score 545.6	DB 14	Length 850
Best Local Similarity	79.1%	Pred. No. 8.3e-105		
Matches 661	Conservative	0	Matches 174	Indels 1
				Gaps 1
151	TCCTCGATTTCTCTCCGGTTTAACTCAGCGCGGCAATATCTACAGTTGATTTTGG 210			
Db	15 TCGCTGAGTTTCCGGCGGTTTCAGACTCAGCGGCGAGCTTCCTTACGTACCAAGCTTTCC 74			
211	GTAAATTTCTTTGAGATCACTACCAAGTATCGTCTCTATTAATGCTATTTGGTCGTGGT 270			
Db	75 GTAACTTTTCAGAGTTACGGCTAAGTATCGTCTCCGATCATGCTATTTGGTCGTGGT 134			
271	CTTATGAGATTTGTCTCTCGGTGTTGAATACGAGACTGAATAGATGGTTGCAGTTAAGA 330			
Db	135 CTTCAGGAATCGTTTGTCTGTTGGTGAATACGGAAGCATAGTTGGTTGTGTGAAGA 194			
331	AAATCGCGAATCGCTTGTGATTTTACATGAGTGTCTAAGAGACTCCGCTGAGATTAAGC 390			
Db	195 AATATCGCAATCGCTTTTGTATTCATATGATGCCAAGGTTACGCTCGTGAGATTTAAGC 254			
391	TCCTCGCCCATTTAAGACCATGAAATGTAAATGGTTTAAAGACGTGATTCCTGCACCT 450			
Db	255 TTCTTAGCATTTAGATCATCATGAAATGTAAATGGTTTAAAGATGTTATTCACACACCT 314			
451	TTCGAAAGGAGTTTCTGATTTTCAATGCTACAGTCACTGCTAGTCACTATGATATCTTCCAC 510			
Db	315 TCGGTATGAGAGTTTATGATGTTTACATACCAACCGAATCATGATGATGATATCTTCCAC 374			
511	AAATATTTGATCCCAACCAAGGTTTATCAGAGATCACTGCTAGTCACTCATGATATCCAGC 570			
Db	375 AAATCATTTGCTCTATATCAAAACCTGTGATGAAACCTGCGCAGTACTTTTGTATACAGA 434			
571	TCCTCCGTGACCTAAATATACATACATTCGCGAATGTTCTTATAGATCTCAAAACCGA 630			
Db	435 TTCTCTCGTGGCTAAGGTATATCATCTTCGCAACATATTCATAGAGATTTGAAACCGA 494			
631	GGAACCTTTGGTAAATGCAATGTGATCTTAAGATATGAGTATGACTTGGTCTGTGAGGC 690			
Db	495 GGAACCTGCTGTTAAATGCAAAATGTGAGCTTAAAGATTTATATTTTGGTCTGTGAGGC 554			
691	CAACATAGAGAACGAGATATGACGGAATATGTTGTATTAACAGATGTTACAGAGCACAG 750			
Db	555 CAACATAGAGAACGATCTTACAGCAAAATATGTTGTACAGAGATGTTATAGGCTCCGTG 614			
751	AGCTTTGTTGAACCTTTCAGATTACACTGCTGTATAGATGTTTGGTCTGTGCGTTGCA 810			
Db	615 AATGTTGTTGAACCTTCAGATTACACTGCTGTATAGATGTTTGGTCTGTGCGTTGCA 674			
811	TCCTATGGAATTTATGAAATAGAAAACCTTTTGGTGGAAACATATCATGATATCAAA 870			
Db	675 TTTTATAGAGCTTATGATATTAAGAAACCTCTGTTTCTGTGGCAAAATCATGTGCAATCAA 734			
871	TACGCTTTTAAACGAGCTTCTTGGCACCCCAACGAGAGCTGATCTT-GAGTTCCTCCAA 929			
Db	735 TCGCGTTATGACAGAGCTTCTTGGCACCTCCAACTGACGCTGATGTTGGGGTTATATAAA 794			
931	AATGAAGATGCAAGAGATACATCAGGCACTCCCAACAATCTTCGCGACAGCATTT 985			
Db	795 AATGACGATGCGAAGAGATATATTCGACAAACTTCTCTAGTATCCGTCGTAACCTTT 850			

ACCESSION	AY108471
VERSION	AY108471.1
KEYWORDS	HTC.
SOURCE	Zea mays.
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
REFERENCE	1 (bases 1 to 1715) Haines,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesilt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes Unpublished (2002) 2 (bases 1 to 1715) Coe,E.C.
JOURNAL	Direct Submission
REFERENCE	Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
TITLE	Location/Qualifiers
AUTHORS	1..1715
JOURNAL	/organism="Zea mays"
FEATURES	/db_xref="maizedb:638497"
source	/db_xref="taxon:4577"
	/clone="PCO143674"
	/clone_11b="Maize Mapping Project/Dupont Consensus Library"
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"
BASE COUNT	445 a 428 c 393 g 449 t
ORIGIN	
Query Match	31.6% Score 545.4; DB 11; Length 1715;
Best Local Similarity	69.9%; Pred. No. 8,5e+105;
Matches 751:	Conservative 0; Mismatches 321; Indels 3; Gaps 1
OY	172 TAACTACGGCGGCAAGATATGTACAGTTTGAATTATTTTGTAATTTCTTTAGATCACTA 231
Db	207 TCAGCCAGGTCGCCGCTTCATCCAGTACAACATCTTCGCAGACGCTTCGAGGTCACT 266
OY	232 CCAAGTATCGTCTCTTATATGCTTATTTGGTCGTGTCCTTAGGAATTTGCTGCTGG 291
Db	267 CCMAATACAAAGCCCCCATCTCCCACATCGGCAAGGGCCCTACGGCATCTGCTGCTGG 326
OY	292 TGTTGAATACGAGCGTAATGAGATGGTTGTCAGTTAAGAATAATTCGGATGCGTTTGATA 351
Db	327 CGCTCAACTCCGAGACGGCAGAGCGAGGTGGCATCAAGAAGATTCGCCAACGCTTCGAKA 386
OY	352 TTTACATGAGATCTAAGAGGACTCTCCGTGAGATTAAAGCTCTCCGCCATTTAGACCATG 411
Db	387 ACAAGATGATGTCCAAAGCGCACGCTCCGGAGATCAAGTCTCCGCCACATGAGACCAAG 446
OY	412 AAAATGTAATGGTTAAGAGACGATGCTCCGCCACCCCTTAGGAAGGGGCTTTTCGANG 471
Db	447 AGAATATGTTGTCATTAAGAGATATCATCTCTCTCCATTGGAGGAGCATTCATCATGATG 506
OY	472 TTTCATCTGCTACTGAACTGATGATGATCTTCACCAAAATTAATTAGATCCAACCAAG 531
Db	507 TGTATATGCGCATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 566
OY	532 GTTTATCAGAGATACAGTCTGACTTATCATCATGAGTCTCTCCGTGAGCTTAANAATACA 591
Db	567 CTTTGTCAGAGGAGACGTGCTGATTTTTCTTTATCAAAATTTCTGCTGCTGGAAGTATA 626
OY	592 TACATTCGCGGATCTTTCTTCATAGAGATCTTAACCGGCAACCTTTTGGAAATGCA 651
Db	627 TACATTCGCAAAATTTCTTCACGCTGATGAGACCTTAGCAATTTCTTTTGAATGCA 686
OY	652 ATTGTGATCTTAAGATATGTGACTTTGGTCTTGATAGGCCAAAACATAGAGAAGAAATA 711

[illegible]

QY 652 ATTGTGATCTTAAGATATGTGATCTTGTCTGTAGCCCAACATAGAGACAGATA 711
 |||||
 Db 535 ATTGTGATCTTAAGATATGTGATCTTGTCTGTAGCCCAACATAGAGACAGATA 594
 |||||

QY 712 TGACGAATATGTTGTAAACAGATGTACAGGCA 746
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 Db 595 TGACGAATATGTTGTAAACAGATGTACAGGCA 629
 |||||

RESULT 7
 B0507523 603 bp mRNA linear EST 22-JUL-2002
 LOCUS EST614938 Generation of a set of potato cDNA clones for microarray
 DEFINITION analyses mixed potato tissues Solanum tuberosum cDNA clone STMG087
 5' end, mRNA sequence.
 ACCESSION B0507523
 VERSION B0507523.2 GI:21923349
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 603)
 REFERENCE Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C.,
 AUTHORS Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
 Karanayeva,S.A.
 TITLE Generation of a set of potato cDNA clones for microarray analyses
 JOURNAL Unpublished (2002)
 COMMENT On Jun 10, 2002 this sequence version replaced gi:21366392.
 Other_ESTS: EST614939
 Contact: Robin Buell
 The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potatodetgr.org
 This clone is available through the Research Genetics, contact the
 Research Genetics for further information 1-800-711-6195 or
 cdna@resgen.com
 Seq primer: T3.
 location/Qualifiers
 1..603
 /organism="Solanum tuberosum"
 /cultivar="Kennebec or Blinje"
 /db_xref="taxon:4113"
 /clone="STMG087"
 /clone_1b="Generation of a set of potato cDNA clones for
 microarray analyses mixed potato tissues"
 /tissue_type="mixed tissues"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; supplier: Combination of untreated and Phytophthora
 infestans-treated libraries of stolons, leaves, leaflets,
 axillary buds of stem explants, petioles, germinating eyes
 tubers, or roots."
 BASE COUNT 178 a 131 c 127 g 167 t
 ORIGIN

Query Match 29.2%; Score 503.4; DB 14; Length 603;
 Best local Similarity 89.9%; Pred. No. 6,7e-96;
 Matches 540; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 670 GTGACTTGTGCTTGTAGGCAACATAGAGAGAAATATGAGAAATATGTGTA 729
 |||||
 Db 2 GTGATTTGTGCTTGTAGGCAACATAGAGAGAAATATGAGAAATATGTAGTA 61
 |||||

QY 730 CCAGATGTATACAGGACACAGAGCTTTGTGAACCTCTTACATACATGCTCTATAG 789
 |||||
 Db 62 CCAGATGTATACAGGACACAGAGCTTTGTGAACCTCTTACATACATGCTCTATAG 121
 |||||

QY 790 ATGTTTGTGCTGTCGATCTTCAATGAACTTATGAAATAGAAACCTTTGTTGTTG 849
 |||||
 Db 122 ATGTTTGTGCTGTCGATCTTCAATGAACTTATGAAATAGAAACCTTTGTTGCTG 181
 |||||

QY 850 GAAAGATCATGTATCATCAATATACCTTGTAAACGAGCTTCTGGACCCCAAGAG 909
 |||||
 Db 182 GAAAGATCATGTATCATCAATATACCTTGTAAACGAGCTTCTGGACCCCAAGAT 241
 |||||

QY 910 CTGATCTGTGCTTCTCCAAATATGAGATGCAAGAGATCATATGAGCAATCCCAAC 969
 |||||
 Db 242 CTGATCTGTAGCTTCTCCGAAATGAGATGCAAAATATATGTCAGCAATCCCAAC 301
 |||||

QY 970 ATCTGCGCAGCAATTTAGCAAGATTTTCCCTCATGTGAACCCATGATATGATCTTG 1029
 |||||
 Db 302 ATCTGCGCAGCAATTTAGCAAGATTTTCCCTCATGTGAACCCATGATATGATCTTG 361
 |||||

QY 1030 TCGATTAATATGTTGACATTCCTACTAGAAATATTAAGATGAGAAACATTAATC 1089
 |||||
 Db 362 TAGATTAATATGTTGACATTCCTACTAGAAATATTAAGATGAGAAACATTAATC 421
 |||||

QY 1090 ATCCCTACCTTGGCAAGCTCCAGATCAGATGAGTGAACCGATGCTCCCTGTTCAATCT 1149
 |||||
 Db 422 ATCCCTACCTTGGCAAGCTCCAGATCAGATGAGTGAACCGATGCTCCCTGTTCAATCT 481
 |||||

QY 1150 CCTTGAATTTGACCAACAGATATAGAGAGCAAAATTAAGACATGATATATCAGG 1209
 |||||
 Db 482 CCTTGAATTTGACCAACAGATATAGAGAGCAAAATTAAGACATGATATATCAGG 541
 |||||

QY 1210 AAGCTTTGATCATGATCTGATATATCTTAAACATTAAGAGAAATCAATTTCTTCTCC 1269
 |||||
 Db 542 AAGCTTTGATCATGATCTGATATATCTTAAACATTAAGAGAAATCAATTTCTTCTCC 601
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QY 1270 T 1270
 Db 602 T 602

RESULT 8
 B6597996 675 bp mRNA linear EST 12-APR-2001
 LOCUS EST496674 cSTS Solanum tuberosum cDNA clone cSTS19121 5' sequence.
 DEFINITION mRNA sequence.
 ACCESSION B6597996
 VERSION B6597996.1 GI:13616136
 KEYWORDS EST.
 SOURCE potato.
 ORGANISM Solanum tuberosum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 1 (bases 1 to 675)
 REFERENCE van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chienlingo,A.,
 AUTHORS Bougri,O., Buell,C.R., Konning,C., Tanksley,S. and Baker,B.
 TITLE Generations of ESTs from sprouting potato eyes
 JOURNAL Unpublished (2000)
 COMMENT The Institute for Genomic Research
 For clone info, please contact Research Genetics, Libraries
 Division tel 1-800-711-6195, email cdna@resgen.com
 Seq primer: M13F-R.
 location/Qualifiers
 1..675
 /organism="Solanum tuberosum"
 /cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="cSTS19121"
 /clone_1b="cSTS"
 /tissue_type="sprouting eyes from tubers"
 /dev_stage="12-14 weeks post harvest"
 /lab_host="SOLR"
 /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
 XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
 taken from tubers. The tubers were incubated at 26C in the
 dark for 2-3 weeks prior to sprouting. The eyes were
 frozen in liquid nitrogen immediately upon removal from
 tubers."
 BASE COUNT 192 a 149 c 137 g 197 t

DEFINITION	Zea mays PCO138354 mRNA sequence.
ACCESSION	AY105588
VERSION	AY105588.1
KEYWORDS	HTC.
SOURCE	Zea mays.
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 1705) Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL	Unpublished (2002)
REFERENCE	2 (bases 1 to 1705)
AUTHORS	Coe,E.C.
TITLE	Direct Submission
JOURNAL	Submitted (25-Apr-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
FEATURES	Location/Qualifiers
source	1..1705 /organism="Zea mays" /db_xref="MaizeDB:638122" /db_xref="taxon:4577" /clone="PCO138354" /clone_id="Maize Mapping Project/DuPont Consensus Library" /note="this sequence is part of a project of EST assemblies resulting from the application of public configs to seed Dupont configs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACS in conjunction with the Maize Mapping Project"
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ORIGIN	
Query Match	27.3%; Score 471; DB 11; Length 1705;
Best Local Similarity	64.8%; Pred. No.3.9e-89;
Matches	699; Conservative 0; Mismatches 380; Indels 0; Gaps 0
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[illegible]

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ORIGIN					
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ACCESSION	AM775829				
VERSION	AM775829.1	GI:775642			
KEYWORDS	EST.				
ORGANISM	Medicago truncatula				
SOURCE	barrel medic.				
REFERENCE	Medicago truncatula				
ORGANISM	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
REFERENCE	Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots:				
REFERENCE	Rosidae, eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;				
REFERENCE	Medicago.				
REFERENCE	1 (bases 1 to 679)				
REFERENCE	Fedorova, M., Pierson, B. L., Samac, D. A., Vance, C. P., Gantt, G. S., Peng				


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Search completed: May 19, 2003, 22:59:20
Job time : 2267 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:23:42 ; Search time 54 Seconds
(without alignments)
669.797 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

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Listing first 45 summaries

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Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	885	44.5	624	9	US-10-072-036-57 Sequence 57, Appl
3	878.5	44.2	360	9	US-10-171-311-127 Sequence 127, App
4	877.5	44.2	604	9	US-10-072-036-59 Sequence 59, Appl
5	877.5	44.2	605	9	US-10-072-036-41 Sequence 41, Appl
6	868	43.7	353	10	US-09-801-368-116 Sequence 116, App
7	868	43.7	435	10	US-09-801-368-150 Sequence 150, App
8	867	43.6	379	9	US-10-059-585-37 Sequence 37, Appl
9	867	43.6	631	9	US-10-072-036-39 Sequence 39, Appl
10	846	42.6	360	9	US-09-918-873-35 Sequence 35, Appl
11	844	42.5	360	9	US-09-918-873-34 Sequence 34, Appl
12	842	42.4	360	9	US-09-918-873-33 Sequence 33, Appl
13	841	42.3	360	9	US-09-918-873-1 Sequence 1, Appl
14	838	42.2	606	9	US-10-072-036-65 Sequence 65, Appl
15	838	42.2	607	9	US-10-072-036-47 Sequence 47, Appl
16	837	42.1	360	9	US-09-918-873-32 Sequence 32, Appl
17	835	42.0	360	9	US-09-918-873-37 Sequence 37, Appl
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27	821	41.3	360	9	US-09-918-873-31	Sequence 31, Appl
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30	794.5	40.0	368	10	US-09-801-368-178	Sequence 269, App
31	653.5	32.9	424	9	US-09-861-097-18	Sequence 18, Appl
32	653.5	32.9	424	9	US-09-861-098-18	Sequence 8, Appl
33	626.5	31.5	422	9	US-09-165-522-5	Sequence 2, Appl
34	626.5	31.5	422	9	US-09-165-522-8	Sequence 269, App
35	626.5	31.5	422	10	US-09-771-161A-269	Sequence 270, App
36	626.5	31.5	422	10	US-09-771-161A-270	Sequence 24, Appl
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39	624.5	31.4	384	9	US-09-861-097-12	Sequence 12, Appl
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41	624.5	31.4	633	9	US-10-072-036-63	Sequence 45, Appl
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ALIGNMENTS

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RESULT 1
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; Sequence 34, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSMALDO DA
; APPLICANT: BOHNER, HANS J
; APPLICANT: THIELEN, NOCH VAN
; APPLICANT: CHEN, RODING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 375
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-34

Query Match          64.8%; Score 1288; DB 10; Length 375;
Best Local Similarity 67.6%; Pred. No. 6.3e-101;
Matches 242; Conservative 46; Mismatches 68; Indels 2; Gaps 1;

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QY 318 ITVEALDHPYLAHLADGDEPICVPVSPFDEQOIGEOIKDVIQAL-SLANE 373
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RESULT 2
US-10-072-036-57
; Sequence 57, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BURON
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072.036
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/417.197
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 57
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MERK1-F64L-S65T-GFP fusion
US-10-072-036-57

Query Match 44.5%; Score 885; DB 9; Length 624;
Best Local Similarity 46.3%; Pred. No. 1.3e-66;
Matches 177; Conservative 72; Mismatches 111; Indels 22; Gaps 7;

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QY 115 REFSVYIAELMDTDLHQIIRSNQGLSEDCQYFMTQLRGLKYIRSHANYLHDLKPSN 174
Db 114 EAMDVYIYODLMDTDYKILKLSQO-LSNDHICYFLYOILRGLKYIRSHANYLHDLKPSN 172
QY 175 LTVANDLITCDGLR---PNIENEN-MTEYVYTKYRAPELLLSSDYTAIDVWSV 230
Db 173 LTVANDLITCDGLR---PNIENEN-MTEYVYTKYRAPELLLSSDYTAIDVWSV 232
QY 231 GCITAEMLNRRKPLFGKDHQVIRLTTELGTPEADLGFQNDADAKRYIRQLPOHPRQO 290
Db 233 GCITAEMLNRRKPLFGKDHQVIRLTTELGTPEADLGFQNDADAKRYIRQLPOHPRQO 292
QY 291 LAEVPVNPALIDLVKMLFFDPTRRITVEALDHPYLAHLADGDEPICVPVSPFDE 350
Db 293 WAKLFPSKSKALDLDRLMTFNPKNRITYEALAHYLBQYPTDPEVAEEPFETDME 352
QY 351 QOIGEOIKDVIQALSLNPE 372
Db 353 LDDLPKRLKELIFQETARPOF 374

RESULT 3
```

```

US-10-171-311-127
; Sequence 127, Application US/10171311
; Publication No. US20030082720A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamackar, Shubhangi
; APPLICANT: Glatz, Karen
; APPLICANT: Ganavaram, Manjula
; APPLICANT: Hoersch, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-127

Query Match 44.2%; Score 878.5; DB 9; Length 360;
Best Local Similarity 48.6%; Pred. No. 2.3e-66;
Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;

QY 33 GNFEITTKYRPPIMPICRGAGYGVSVLNTLNEVAVKINAPDIYMDAKRTLRK 92
Db 16 GQVDFVGPVRY-TNLSYIGEGAGYGVSVLNTLNEVAVKINAPDIYMDAKRTLRK 73
QY 93 LRLHLDHENYVIGRDVTPPLRREFSDVYIATLMDTDLHQIIRSNQGLSEDCQYFMTQ 152
Db 74 LRLHLDHENYVIGRDVTPPLRREFSDVYIATLMDTDLHQIIRSNQGLSEDCQYFMTQ 132
QY 153 LRLGLKYIRSHANYLHDLKPSNLIVNANCDIKCDFGLAR---PNIENEN-MTEYVYTK 208
Db 133 LRLGLKYIRSHANYLHDLKPSNLIVNANCDIKCDFGLAR---PNIENEN-MTEYVYTK 192
QY 209 YRAPELLNNSDYTAIDVWSVGCIFMELNRRKPLFGKDHQVIRLTTELGTPEADL 268
Db 193 YRAPELLNNSDYTAIDVWSVGCIFMELNRRKPLFGKDHQVIRLTTELGTPEADL 252
QY 269 GFLONEDAKRYIRQLPOHPRQOALAEVFPVNPALIDLVKMLFFDPTRRITVEALDHPY 328
Db 253 NCILNKAARYLTLSPKRNKVPVNPALIDLVKMLFFDPTRRITVEALDHPY 312
QY 329 LAKHDAGDEPICVPVSPFDEQOIGEOIKDVIQALSLNPE 374
Db 313 LEQYDPSDEPIAEAPKPFMEIDLDPKRLKELIFEETARFOG 358

RESULT 4
US-10-072-036-59
; Sequence 59, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BURON
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kurt SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
```

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FILE REFERENCE: 3759-0120P
CURRENT APPLICATION NUMBER: US/10/072.036
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/417,197
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 59
LENGTH: 604
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Efk2-EGFP fusion
US-10-072-036-59

Query Match
Best Local Similarity 44.2%; Score 877.5; DB 9; Length 604;
Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;

QY 33 GNFEITTKYRPIMPICRGAYGIVCSVLNTELMNEMAVKRIANAFDIYMDAKRLREIK 92
DB 14 GQVEDVGRY-TNLSYIGGAYGWCASAYDNLNKVRVAIKKI-SPEHOTYQORLREIK 71
QY 93 LLRLDHEENVIGLRDVIPEPLRREFSDYIATELMDTDLHOIIRSNQGLSEDHCOYFMQ 152
DB 72 LLRRHENIIGINDIIRAPTEQMKDVIYQDLMETDLYKLKT-QHLSNDHICYFLXQ 130
QY 153 LLRLGKYHSANVLRDLKPSNLLVANCDLKICDFGLAR--PNIENEN-MTEYVYTRM 208
DB 131 ILRGLKYHSANVLRDLKPSNLLNTCDLKICDFGLARVADPDHDHGTLEEVATRM 190
QY 209 YRAPELLNSSDYTAIDWVSVCIFMELMNRKPLFGGKDHYHQIRLLTELGTPTEDL 268
DB 191 YRAPEIMLNSKGYTSIDWVSVCILAEMLSNRPFPGKHLYDQNLHIGIGSPQEDL 250
QY 269 GFLONEDAKRYIRQLPQHPROQLAEVPPHVNPLAIDLVDKMLTFDPTRITVEEALDHPY 328
DB 251 NCIIILKARNYLSLPHNKKVPMNRLFVNADSKALDLDKMLTFMHRKRIEVEQALAHPY 310
QY 329 LAKLHDAGDEPICVPFSEFEOGIGEOIKDMITYQEALSINPEY 374
DB 311 LEQYDPSDEPIAEAPFKFDMELDDLPRKELKELIFEETARQPGY 356

RESULT 5
US-10-072-036-41
Sequence 41, Application US/10072036
Publication No. US20030082564A1
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP
APPLICANT: Sara BJORN
APPLICANT: Soren TULLIN
APPLICANT: Kasper ALMHOLT
APPLICANT: Kurt SCUDDER
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
FILE REFERENCE: 3759-0120P
CURRENT APPLICATION NUMBER: US/10/072.036
CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/417,197
PRIOR FILING DATE: 1999-10-07
NUMBER OF SEQ ID NOS: 143
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 605
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EGFP-Erk2 fusion
US-10-072-036-41

Query Match
Best Local Similarity 44.2%; Score 877.5; DB 9; Length 605;
Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;
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Matches 168; Conservative 69; Mismatches 102; Indels 7; Gaps 5;

QY 33 GNFEITTKYRPIMPICRGAYGIVCSVLNTELMNEMAVKRIANAFDIYMDAKRLREIK 92
DB 261 GQVEDVGRY-TNLSYIGGAYGWCASAYDNLNKVRVAIKKI-SPEHOTYQORLREIK 318
QY 93 LLRLDHEENVIGLRDVIPEPLRREFSDYIATELMDTDLHOIIRSNQGLSEDHCOYFMQ 152
DB 319 LLRRHENIIGINDIIRAPTEQMKDVIYQDLMETDLYKLKT-QHLSNDHICYFLXQ 377
QY 153 LLRLGKYHSANVLRDLKPSNLLVANCDLKICDFGLAR--PNIENEN-MTEYVYTRM 208
DB 378 ILRGLKYHSANVLRDLKPSNLLNTCDLKICDFGLARVADPDHDHGTLEEVATRM 437
QY 209 YRAPELLNSSDYTAIDWVSVCIFMELMNRKPLFGGKDHYHQIRLLTELGTPTEDL 268
DB 438 YRAPEIMLNSKGYTSIDWVSVCILAEMLSNRPFPGKHLYDQNLHIGIGSPQEDL 497
QY 269 GFLONEDAKRYIRQLPQHPROQLAEVPPHVNPLAIDLVDKMLTFDPTRITVEEALDHPY 328
DB 498 NCIIILKARNYLSLPHNKKVPMNRLFVNADSKALDLDKMLTFMHRKRIEVEQALAHPY 557
QY 329 LAKLHDAGDEPICVPFSEFEOGIGEOIKDMITYQEALSINPEY 374
DB 558 LEQYDPSDEPIAEAPFKFDMELDDLPRKELKELIFEETARQPGY 603

RESULT 6
US-09-801-368-116
Sequence 116, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary
APPLICANT: Milne, Todd
APPLICANT: NO. US20020128250A1man, Thea
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801.368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 116
LENGTH: 353
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-116

Query Match
Best Local Similarity 43.7%; Score 868; DB 10; Length 353;
Matches 167; Conservative 61; Mismatches 91; Indels 18; Gaps 5;

QY 49 IGRGAYGIVCSVLNTELMNEMAVKRIANAFDIYMDAKRLREIKLLRLDHEENVIGLRDV 108
DB 19 LGEAGAYGVCATHRKPTGEIYAIKKI-EPPDKPLALTRLRIKILKHKHENITIFNI 77
QY 109 IPPPLRREFSDYIATELMDTDLHOIIRSNQGLSEDHCOYFMQQLRLGKYHSANVLR 168
DB 78 QRPDSFENFENYIIQELMQDLDLHRYI-STQMLSDHIOYFIYQIRLRAVKVYHGSNVIR 136
```

[illegible]

```

RESULT 7
US-09-801-368-150
: Sequence 150. Application US/09801368
: Patent No. US20020128250A1
: GENERAL INFORMATION:
: APPLICANT: Busby, Robert
: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin
: APPLICANT: Maxon, Mary
: APPLICANT: Milne, Todd
: APPLICANT: No. US20020128250A1man, Thea
: APPLICANT: Royer, John
: APPLICANT: Salama, Sofie
: APPLICANT: Sherman, Amir
: APPLICANT: Silva, Jeff
: APPLICANT: Summers, Eric
: TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
: FILE REFERENCE: 109272.147
: CURRENT APPLICATION NUMBER: US/09/801,368
: PRIOR FILING DATE: 2001-03-07
: PRIOR APPLICATION NUMBER: US 09/487,558
: PRIOR FILING DATE: 2000-01-19
: PRIOR APPLICATION NUMBER: US 60/160,587
: PRIOR FILING DATE: 1999-10-20
: NUMBER OF SEQ ID NOS: 440
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 150
: LENGTH: 435
: TYPE: PRF
: ORGANISM: Saccharomyces cerevisiae
: US-09-801-368-150

```

Query Match 43.7%; Score 868; DB 10; Length 435;
 Best Local Similarity 46.9%; Pred. No. 2; 36-65;
 Matches 165; Conservative 68; Mismatches 111; Indels 8; Gaps 4.

Db 233 LGSPKQVINYINIGSENLTKFTSLRPHRDP1PFSRFRFTVEPDADVLEKKMLYDPPKRRIT 292

QY 320 VEFALDHPYLAKLHDAGDEPICPVPSFSEFQOGIGEEQIKDMLYQALSLN 371

Db 293 AADALAHPSYSPHYDPDEPVADAKFQWHEFNDDLLPVDTVRWVMYSSILDFH 344

```

RESULT 8
US-10-059-585-37
: Sequence 37, Application US/1009585
: Publication No. US2003008276A1
: GENERAL INFORMATION:
: APPLICANT: Ota, Toshio
: APPLICANT: Isogai, Takao
: APPLICANT: Nishikawa, Tetsuo
: APPLICANT: Hayashi, Koji
: APPLICANT: Otsuka, Kaoru
: APPLICANT: Yamamoto, Jun-ichi
: APPLICANT: Ishii, Shizuko
: APPLICANT: Sugiyama, Tomoyasu
: APPLICANT: Wakamatsu, Ai
: APPLICANT: Nagai, Keiichi
: APPLICANT: Otsuki, Tetsuji
: APPLICANT: Funahashi, Shin-ichi
: APPLICANT: Senoo, Chiaki
: APPLICANT: Nezu, Jun-ichi
: TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
: TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
: FILE REFERENCE: 06501-098001
: CURRENT APPLICATION NUMBER: US/10/059, 585
: CURRENT FILING DATE: 2002-01-29
: PRIOR APPLICATION NUMBER: PCT/JP00/05060
: PRIOR FILING DATE: 2000-07-28
: PRIOR APPLICATION NUMBER: US 60/183,322
: PRIOR FILING DATE: 2000-02-17
: PRIOR APPLICATION NUMBER: US 60/159,590
: PRIOR FILING DATE: 1999-10-18
: PRIOR APPLICATION NUMBER: JP 2000-118776
: PRIOR FILING DATE: 2000-01-11
: PRIOR APPLICATION NUMBER: JP 2000-183767
: PRIOR FILING DATE: 2000-05-02
: PRIOR APPLICATION NUMBER: JP 11-248036
: NUMBER OF SEQ ID NOS: 64
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 37
: LENGTH: 379
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-059-585-37

```

[illegible]

Db 232 GCILAEMLSNRPIFGKHYLDOLNHLIGLSPSEDNLNCIMKARNYLQSLPSKTKVA 291
QY 291 LAEVPFHPVPLAIDLVKMLTDPTRRTIVEEALDHPYLAKLHADDEPILCPVPSEFDE 350
Db 292 WAKLPKSSKALDLDRLMTFNPKNRTIVEEALHPYLEQYVDPDEVAEPEPFAME 351
QY 351 OOGIGEJOIKMDIYOEALSLNP 372
Db 352 LDDPKERLKELIPOETARFOP 373

RESULT 9

US-10-072-036-39
; Sequence 39, Application US/10072036
; Publication No. US20030082564A1
; GENERAL INFORMATION:
; APPLICANT: Ole THASTRUP
; APPLICANT: Sara BJORN
; APPLICANT: Soren TULLIN
; APPLICANT: Kasper ALMHOLT
; APPLICANT: Kuit SCUDDER
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0120P
; CURRENT APPLICATION NUMBER: US/10/072,036
; CURRENT FILING DATE: 2002-09-13
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39
; LENGTH: 631
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-Erk1 fusion construct
US-10-072-036-39

Query Match

Best Local Similarity 45.8%; Score 867; DB 9; Length 631;
Matches 175; Conservative 71; Mismatches 114; Indels 22; Gaps 7;

QY 2 ADANAGAGGQ-----PPDESVLTGCGYVQFDIFGNFETTKYRPPIMIGRAY 54
Db 255 AAAAGGGGGERRRGVPGRVEY-----VKQPPDVGRY-TQLOYTEGAY 305
QY 55 GIVCSVLTLEMDVAVKRIANAFDIYMDAKRTLEIKLLRLDHEHNVGLRDVIPPPLR 114
Db 306 GWSSAYDHVTRKTRVAIKKI-SPEHQTYCQRTLEIQILRLPRHENVIGIRDLKASTL 364
QY 115 REFSVYIATLEMDDDHIIIRSNQGLSEDHCOYFMYQLLRGLKTYHSANVLRDLKPSN 174
Db 365 EAMRVYIYQDLMETDYLKLSQO-LSNDHICYLYQILRGLKTYHSANVLRDLKPSN 423
QY 175 LTVNANCDKICDFGLAR--FNIEEN-ATEYVYTRWRAPPELLNSSDYRAAIDVWGV 230
Db 424 LLSNTTCDKICDFGLARADPEHDTGLTEYVATRWRAPEIMNSGYIKSIDIVSY 483
QY 231 GCIFELMNRKPLFGSGKHVQIRLLTELLGTPTEADLGLFLONEADAKRYIROLPOHPRQO 290
Db 484 GCILAEMLSNRPIFGKHYLDOLNHLIGLSPSEDNLNCIMKARNYLQSLPSKTKVA 543
QY 291 LAEVPFHPVPLAIDLVKMLTDPTRRTIVEEALDHPYLAKLHADDEPILCPVPSEFDE 350
Db 544 WAKLPKSSKALDLDRLMTFNPKNRTIVEEALHPYLEQYVDPDEVAEPEPFAME 603
QY 351 OOGIGEJOIKMDIYOEALSLNP 372
Db 604 LDDPKERLKELIPOETARFOP 625

RESULT 10
US-09-918-873-35

; Sequence 35, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radna, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 360
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: GSK-3/p38 inhibitor binding site chimera
US-09-918-873-35

Query Match

Best Local Similarity 42.6%; Score 846; DB 9; Length 360;
Matches 163; Conservative 65; Mismatches 107; Indels 6; Gaps 5;

QY 36 FETTTYRPPIMIGRATGIVCSVLTLEMDVAVKRIANAFDIYMDAKRTLEIKRLR 95
Db 18 WEVPERYQ-NLSPVGGAGSVCAAFDTGHRVAVKKSRRPQSIHAKRYRELRLK 76
QY 96 HDHENVIGLRDVIIPPPLR-REFSDVYIATLEMDTDHIIIRSNQGLSEDHCOYFMYQL 154
Db 77 HMDHCNVIGLDVYTPARSLSEFNDVYLYTDLMGADLNTVKC-QULTDQVFLYQIL 135
QY 155 RGLKTYHSANVLRDLKPSNLVANCIDKICDFGLARPNIEENNTVEYVTRWRAPEL 214
Db 136 RGLKTYHSADIIHRDLKPSNLAVNEDECELDIFGLARHT--DDEMTGYATRWRAPEI 193
QY 215 LNSSDYTAIDVWSVGCIFELMNRKPLFGGDHGHQIRLLTELLGTPTEADLGLONE 274
Db 194 MLNMWHYNOTVDIWSVGCIMAEILLTGRTLPFGTDHIDQILRLVGTGPAELLKRISSE 253
QY 275 DAKRYIROLPOHPRQOLAEVFPHPVPLAIDLVKMLTDPTRRTIVEEALDHPYLAKLHD 334
Db 254 SARNTYQSLAQMKMFANFYICANPLAYLDLEKMLYDSDKRTTAQALAHAFQYHD 313
QY 335 AGDEPICVPFSEFEOGIGEJOIKMDIYOEALSLNPEYA 375
Db 314 PDDEPVAD-PYDQSFESRDLLIDEMKSLTYDEVISVPPHA 353

RESULT 11

US-09-918-873-34
; Sequence 34, Application US/09918873
; Publication No. US20030032649A1
; GENERAL INFORMATION:
; APPLICANT: Goldsmith, Elizabeth J.
; APPLICANT: Radna, Akella
; APPLICANT: Gaynor, Richard B.
; TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
; FILE REFERENCE: A33864 090495.0232
; CURRENT APPLICATION NUMBER: US/09/918,873
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 360
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: JNK-3/p38 inhibitor binding site chimera
US-09-918-873-34

	Query Match	42.5%	Score	84.4	DB	9	Length	360
	Best Local Similarity	47.9%	Pred	No.1	9e-63			
	Matches	162	Conservative	65	Mismatches	105	Indels	6
								Gaps
								5
QY	36	FEITTKYRPIMPJRGANGIVCSYLTNLTMLNEMVAKKIANAFDIYMDAKRTLEIKLR	95					
Db	18	WEVPERYQ-NLSPVSGAAGVCAFDFTGHRVAKKTLSPFQSIHAKKRYRELRLLK	76					
QY	96	HLIDHENYGLRVPYIPPLR-REFSDVYITELMDYDLHOITRNSOGLSDHCQYFYQLL	154					
Db	77	HNNHKNVIGLDVFEPARSLFEFNYYLTVELTLMGADLNINIVC-OKITDDHVOFLYYQL	135					
QY	155	RLKLTTHSANLHRLDKPKNLTVYANCDLIDCFGLARINENENTEVYTVRWYAPRL	214					
Db	136	RLKLTTHSADLTTHRLDKPKNLAVNEDECKLIDFGLART--DDEKTYVATRWYAPRL	193					
QY	215	LNSSDYTAIDVWSVGCIFMELMNRKPLFGGRDHYHQIRLTTELGPTTEADLGLQNE	274					
Db	194	MLNMYHYQYTDVWSVGCIMALLGRTLFPGLDHDIDCKLILRLVGTGALLKKIISSE	253					
QY	275	DAKRITROLQHPROQLAEVPPHVPRLAIDVYDKMLTPTPTRTIYEEALDHPYAKLKD	334					
Db	254	SARNYIOSLQMPKKNFANVETGANPLAVALLEKMLVLDSDRKTPAALAHAYFOYHD	313					
QY	335	AGDEPTCPVPFSFDEQOIGEEQIKDMYQALSLNP	372					
Db	314	PDDEPVAD-PYQSFESRDLIDEMKSLYYDEVISFP	350					

```

RESULT 12
US-09-918-873-33
: Sequence 33, Application US/09918873
: Publication No. US20030032649A1
GENERAL INFORMATION:
APPLICANT: Goldsmith, Elizabeth J.
APPLICANT: Radna, Akella
APPLICANT: Gaynor, Richard B.
TITLE OF INVENTION: CHIMERIZING PROTEIN KINASES FOR DRUG
TITLE OF INVENTION: DISCOVERY
FILE REFERENCE: A33864 090495.0232
CURRENT APPLICATION NUMBER: US/09/918,873
CURRENT FILING DATE: 2002-07-31
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 33
LENGTH: 360
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: MEK1/P38 inhibitor binding site chimera
US-09-918-873-33

```

[illegible][illegible][illegible]

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RESULT 14
US-10-072-036-65
Sequence 65, Application US/10072036
Publication No. US20030082564A1
GENERAL INFORMATION:
APPLICANT: Ole THASTRUP
APPLICANT: Sara BJRON
APPLICANT: Soren TULLIN
APPLICANT: Kasper ALMHOLT
APPLICANT: Kurt SCUDDER
TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To A
TITLE OF INVENTION: On A Cellular Response
FILE REFERENCE: 3759-0120P
CURRENT APPLICATION NUMBER: US/10/072.036
CURRENT FILING DATE: 2002-09-13

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: PRIOR APPLICATION NUMBER: 09/417,197
: PRIOR FILING DATE: 1999-10-07
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 65
: LENGTH: 606
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: p38-EGFP fusion
US-10-072-036-65

```

```

Query Match          42.2%; Score 838; DB 9; Length 606;
Best Local Similarity 47.9%; Pred. No. 1.2e-62;
Matches 162; Conservative 63; Mismatches 107; Indels 6; Gaps 5;

```

```

QY 36 FEITTKYRPPIMPGRGAGIVCSVLNTELMNMAVAKKIANAFDIYMDAKRTLRREIKLLR 95
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 18 WEVPERYQ-NLSPVSGAAGVCAAFDFTGRLVAVKKLSRPFQSIHAKRTYRELRLIK 76
QY 96 HLDHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNGLSDHCQYEMYQL 154
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 77 HMKHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNGLSDHCQYEMYQL 135
QY 155 RGLKTIHSADIIHRDLKPSNLLVANNCDLKICDFGLARPINENMTEVYTRWYRAPET 214
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 RGLKTIHSADIIHRDLKPSNLLVANNCDLKICDFGLARPINENMTEVYTRWYRAPET 193
QY 215 LINSDDYTAIDVWSVGCIFMELMNRKPLFGSKDHYHQIRLTTELGTPTTEADLGFONE 274
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 194 MLNMMHYNOTVDIWSVGCIMAEELTGRLEPCTDHDQKLILRLVGTGAEELKKISSE 253
QY 275 DAKRYIROLPOHPRQOLAEVFPVNPALDLDVKMLTPTPTRIYVEALDHPYLAKLHD 334
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 254 SARNTYIOSLTQMPKMFANVFIGNAPLAVDLLEKMLVLDSDKRITPAQALAHAYFAQYHD 313
QY 335 AGDEPICVPFSPDFEPOGIGEGQIKDMITYOELSLNP 372
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 314 PDDEPVAD-PYDQSFESRDLIDEMKSLTYDEVISFVP 350

```

```

RESULT 15
US-10-072-036-47
: Sequence 47, Application US/10072036
: Publication No. US20030082564A1
: GENERAL INFORMATION:
: APPLICANT: Ole THASTRUP
: APPLICANT: Sara BJORN
: APPLICANT: Soren TULLIN
: APPLICANT: Kasper ALMHOLT
: APPLICANT: Kurt SCUDDER
: TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
: FILE REFERENCE: 3/59-0120P
: CURRENT APPLICATION NUMBER: US/10/072,036
: PRIOR FILING DATE: 2002-09-13
: PRIOR APPLICATION NUMBER: 09/417,197
: NUMBER OF SEQ ID NOS: 143
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 47
: LENGTH: 607
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: EGFP-p38 fusion
US-10-072-036-47

```

```

Query Match          42.2%; Score 838; DB 9; Length 607;
Best Local Similarity 47.9%; Pred. No. 1.2e-62;
Matches 162; Conservative 63; Mismatches 107; Indels 6; Gaps 5;

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```

Db 265 WEVPERYQ-NLSPVSGAAGVCAAFDFTGRLVAVKKLSRPFQSIHAKRTYRELRLIK 323
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 96 HLDHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNGLSDHCQYEMYQL 154
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 HMKHENVIGLRDVIPTPLR-REFSDVYIATELMDTDLHOIISNGLSDHCQYEMYQL 382
QY 155 RGLKTIHSADIIHRDLKPSNLLVANNCDLKICDFGLARPINENMTEVYTRWYRAPET 214
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 383 RGLKTIHSADIIHRDLKPSNLLVANNCDLKICDFGLARPINENMTEVYTRWYRAPET 440
QY 215 LINSDDYTAIDVWSVGCIFMELMNRKPLFGSKDHYHQIRLTTELGTPTTEADLGFONE 274
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 441 MLNMMHYNOTVDIWSVGCIMAEELTGRLEPCTDHDQKLILRLVGTGAEELKKISSE 500
QY 275 DAKRYIROLPOHPRQOLAEVFPVNPALDLDVKMLTPTPTRIYVEALDHPYLAKLHD 334
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 501 SARNTYIOSLTQMPKMFANVFIGNAPLAVDLLEKMLVLDSDKRITPAQALAHAYFAQYHD 560
QY 335 AGDEPICVPFSPDFEPOGIGEGQIKDMITYOELSLNP 372
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 561 PDDEPVAD-PYDQSFESRDLIDEMKSLTYDEVISFVP 597

```

```

Search completed: May 20, 2003, 00:31:55
Job time : 56 secs

```


GenCore version 5.1.5
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 20, 2003, 00:16:27 ; Search time 43 Seconds
(without alignments)
838.362 Million cell updates/sec

Title: US-09-623-034-2

Perfect score: 1987

Sequence: 1 MADANMGAGGQFPDPSPVL.....EQGIKDMYGEALSLNPEYA 375

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	2	T03971
2	1662	83.6	370	2	T47504
3	1661	83.6	370	2	S40469
4	1650	83.0	371	2	T14915
5	1634	82.2	371	2	T09622
6	1509	75.9	393	2	S51321
7	1500.5	75.5	387	2	S48123
8	1498.5	75.4	394	2	S33635
9	1498.5	75.4	395	2	S40472
10	1473	74.1	369	2	S56638
11	1340.5	67.5	376	2	S40470
12	1308	65.8	371	2	S60121
13	1292	65.0	371	2	S51330
14	1285	64.7	363	2	C86214
15	1279.5	64.4	393	2	T47803
16	1274	64.1	376	2	S40471
17	1258.5	63.3	369	2	C86146
18	1244.5	62.6	373	2	T13024
19	1219	61.3	406	2	D84898
20	1094.5	55.1	372	2	S39559
21	1078	54.3	370	2	F86236
22	1075.5	54.1	384	2	S52989
23	1069	53.8	376	2	F96619
24	1061	53.4	376	2	B84561
25	1052	52.9	368	2	S40473
26	1029.5	51.8	415	2	A56042
27	1002	50.4	361	2	C85430
28	924	46.5	356	2	T51944
29	900.5	45.3	361	2	T51943

30	896.5	45.1	376	2	A36978	MAP kinase mpk-1 (
31	896.5	45.1	444	2	A36977	MAP kinase sur-1 (
32	885	44.5	377	2	S28184	Ca2+/calmodulin-de
33	884.5	44.5	369	2	JW0053	extracellular sign
34	883	44.4	380	2	JC1451	Ca2+/calmodulin-de
35	879	44.2	392	2	JW0052	extracellular sign
36	878.5	44.2	360	1	J01400	MAP kinase 1 (EC 2
37	878	44.2	815	2	B56708	extracellular sign
38	877.5	44.2	358	2	S16444	mitogen-activated
39	877.5	44.2	358	2	A40033	protein kinase (EC
40	877.5	44.2	360	2	S25011	protein kinase ERK
41	877.5	44.2	369	2	A60041	Ca2+/calmodulin-de
42	875	44.0	349	2	S68675	mitogen-activated
43	872	43.9	372	2	S15663	protein kinase (EC
44	871.5	43.9	361	2	A37584	mitogen-activated
45	868	43.7	353	2	S28548	protein kinase (EC

ALIGNMENTS

RESULT 1

T03971
mitogen-activated protein kinase (EC 2.7.1.-) WIPK - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T03971
R:Seo, S.; Okamoto, M.; Seto, H.; Ishizuka, K.; Sano, H.; Ohashi, Y.
Science 270, 1988-1992, 1995
A:Title: Tobacco MAP kinase: a possible mediator in wound signal transduction pathway
A:Reference number: 215170; PMID:96123271; PMID:8533090
A:Accession: T03971
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-375 <SEO>
A:Cross-References: EMBL:D61377; NID:g1136297; PIDN:BAA09600.1; PID:g1136298
C:Comment: MAP kinase is part of the initial response of higher plants to mechanical
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase
F:40-329/Domain: protein kinase homology <KIN>

Query Match	100.0%;	Score 1987;	DB 2;	Length 375;
Best Local Similarity	100.0%;	Pred. No. 9.7e-89;		
Matches 375;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MADANMGAGGQFPDPSPVLTHGGQYVQDFGNGFEITTKYRPPIPIGRGAYGIVCSV	60	
DB	1	MADANMGAGGQFPDPSPVLTHGGQYVQDFGNGFEITTKYRPPIPIGRGAYGIVCSV	60	
QY	61	LMTLLENVAVKKNAPFIYMDAKRTLEIKLRLHLEHNYIGLADYIPPLRRFSNV	120	
DB	61	LMTLLENVAVKKNAPFIYMDAKRTLEIKLRLHLEHNYIGLADYIPPLRRFSNV	120	
QY	121	YATLMTDLDLQIIRSNGLSEDCQYFMYOLLRLGKTYHSANVYLRDLKSNLLNVNN	180	
DB	121	YATLMTDLDLQIIRSNGLSEDCQYFMYOLLRLGKTYHSANVYLRDLKSNLLNVNN	180	
QY	181	CDLKICDEGLARPNIENENKTEYVVTWYRAPELLNNSDYPAADVWSGCIPELMNR	240	
DB	181	CDLKICDEGLARPNIENENKTEYVVTWYRAPELLNNSDYPAADVWSGCIPELMNR	240	
QY	241	KPLFGKHVHDIRLTLLTGTPTEADLGEFQNEAKRYIRQLPQHPROQLAEVPHVNP	300	
DB	241	KPLFGKHVHDIRLTLLTGTPTEADLGEFQNEAKRYIRQLPQHPROQLAEVPHVNP	300	
QY	301	LAIDLVDKMLTFDPTTRITVEEALDHPYLAKLHDAAGDEPICVPSFDEQOGIGEEQIK	360	
DB	301	LAIDLVDKMLTFDPTTRITVEEALDHPYLAKLHDAAGDEPICVPSFDEQOGIGEEQIK	360	
QY	361	DMITVOEALSLNPEYA 375		
DB	361	DMITVOEALSLNPEYA 375		

RESULT 2
T47504

mitogen-activated protein kinase 3 - Arabidopsis thaliana

N:Alternate names: protein F9K21.220

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence, revision 20-Apr-2000 #text, change 19-May-2000

C:Accession: T47504

R:Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unsel, M.; Mewes, H.W.; Lemcke, K. submitted to the Protein Sequence Database, February 2000

A:Reference number: 224467

A:Accession: T47504

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-370 <JOR>

A:Cross-references: EMBL:AL18657

A:Experimental source: cultivar Columbia; BAC clone F9K21

C:Genetics:

A:Map position: 3

A:Insertions: 53/2; 96/3; 142/3; 253/3; 315/1

A:Note: F9K21.220

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 83.6%; Score 1662; DB 2; Length 370;

Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGQPPDPSPVLTGCGVYVDFGPFETTKYRPPIMPICRGAYGVCVLTNEL 65

Db 1 MNTGGQYTDPAVATHGQGFISYDIFGSLFEITSKYRPIPIIGRGAYGVCVLTDEL 60

QY 66 NEMVAKKIANAFDIYDAKTLREIKLRHLDHENVIGLNDVIPPRLRPSDYATL 125

Db 61 NELVAMKKIANAFDNDMAKRTLRKLRHLDHENVIGLNDVIPPRLRPSDYATL 120

QY 126 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 185

Db 121 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 180

QY 186 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFG 245

Db 181 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFP 240

QY 246 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 305

Db 241 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 300

QY 306 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPICVPFSPFDEPOGIGSEOTKDMYQ 365

Db 301 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPICVPFSPFDEPOGIGSEOTKDMYQ 360

QY 366 EALSLNPEY 374

Db 361 EALSLNPEY 369

RESULT 3

S40469

mitogen-activated protein kinase 3 (EC 2.7.1.-) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 06-Oct-1994 #sequence, revision 19-Jan-1996 #text, change 20-Jun-2000

C:Accession: S40469

R:Mizoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.

FEBS Lett. 336, 440-444, 1993

A:Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.

A:Reference number: S40469; MUID:94109583; PMID:8282107

A:Accession: S40469

A:Molecule type: mRNA

A:Residues: 1-370 <MIZ>

A:Cross-references: EMBL:DJ1839; NID:94573397; PIDN:BA04866.1; PID:94573398

C:Genetics:

A:Gene: MPK3

C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match

Best Local Similarity 82.4%; Score 1662; DB 2; Length 370;

Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGQPPDPSPVLTGCGVYVDFGPFETTKYRPPIMPICRGAYGVCVLTNEL 65

Db 1 MNTGGQYTDPAVATHGQGFISYDIFGSLFEITSKYRPIPIIGRGAYGVCVLTDEL 60

QY 66 NEMVAKKIANAFDIYDAKTLREIKLRHLDHENVIGLNDVIPPRLRPSDYATL 125

Db 61 NELVAMKKIANAFDNDMAKRTLRKLRHLDHENVIGLNDVIPPRLRPSDYATL 120

QY 126 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 185

Db 121 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 180

QY 186 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFG 245

Db 181 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFP 240

QY 246 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 305

Db 241 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 300

QY 306 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPICVPFSPFDEPOGIGSEOTKDMYQ 365

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:35-324/Domain: protein kinase homology <KIN>
F:44-52/Region: protein kinase ATP-binding motif

Query Match

Best Local Similarity 83.6%; Score 1661; DB 2; Length 370;

Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGQPPDPSPVLTGCGVYVDFGPFETTKYRPPIMPICRGAYGVCVLTNEL 65

Db 1 MNTGGQYTDPAVATHGQGFISYDIFGSLFEITSKYRPIPIIGRGAYGVCVLTDEL 60

QY 66 NEMVAKKIANAFDIYDAKTLREIKLRHLDHENVIGLNDVIPPRLRPSDYATL 125

Db 61 NELVAMKKIANAFDNDMAKRTLRKLRHLDHENVIGLNDVIPPRLRPSDYATL 120

QY 126 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 185

Db 121 LMDTDLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 180

QY 186 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFG 245

Db 181 CDFGLARPNENMTEVYTRWYRAPPELLNNSDYTAIDVWSYGCIFMELMNRKPLFP 240

QY 246 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 305

Db 241 GKDHVQIRLTTELGTPTTEADLGFLOEDAKRYIRQLPQHPROQLAEVPHVNPALIDL 300

QY 306 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPICVPFSPFDEPOGIGSEOTKDMYQ 365

Db 301 VDKMLTDPPTRRITVEALDHPYLAKLHDADDEPICVPFSPFDEPOGIGSEOTKDMYQ 360

QY 366 EALSLNPEY 374

Db 361 EALSLNPEY 369

RESULT 4

T14915

mitogen-activated protein kinase I (EC 2.7.1.-) - parsley

N:Alternate names: MAP kinase I

C:Species: Petroselinum crispum (parsley)

C:Date: 20-Sep-1999 #sequence, revision 20-Sep-1999 #text, change 21-Jul-2000

C:Accession: T14915

R:Ligterink, W.; Kroj, T.; zur Nieden, U.; Hirt, H.; Scheel, D.

Science 276, 2054-2057, 1997

A:Title: Receptor-mediated activation of a MAP kinase in pathogen defense of plants.

A:Reference number: 218265; MUID:97342856; PMID:9197271

A:Accession: T14915

A:Molecule type: translated from GB/EMBL/DBJ

A:Status: preliminary

A:Residues: 1-371 <LIG>

A:Cross-references: EMBL:Y12785; NID:92231033; PIDN:CAA73323.1; PID:92231034

C:Comment: MAP kinase is part of the initial response of higher plants to mechanical

C:Superfamily: kinase-related transforming protein; protein kinase homology

C:Keywords: ATP; phosphotransferase

F:36-325/Domain: protein kinase homology <KIN>

Query Match

Best Local Similarity 83.0%; Score 1650; DB 2; Length 371;

Matches 300; Conservative 39; Mismatches 28; Indels 0; Gaps 0;

QY 9 GCGQPPDPSPVLTGCGVYVDFGPFETTKYRPPIMPICRGAYGVCVLTNELNM 68

Db 5 GCGQYTDPAVATHGQGFISYDIFGSLFEITSKYRPIPIIGRGAYGVCVLTDEL 64

QY 69 VAVKIANAFDIYDAKTLREIKLRHLDHENVIGLNDVIPPRLRPSDYATLMD 128

Db 65 VAVKIANAFDIYDAKTLREIKLRHLDHENVIGLNDVIPPRLRPSDYATLMD 124

QY 129 TDHLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 188

Db 125 TDHLHOIIRSNGLSEHCOYFYLQRLGKLYHSANVLRDLKPSNLLNANCDLKI 184

```

OY 189 GLARPNIENENETEVYTRWYRAPPELLNSSDYTAIDVWSVGCIFMELMNKRPLEGGKD 248
    ||| | :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 185 GLARNINTDEFETEVYTRWYRAPPELLNSSDYTAIDVWSVGCIFMELMNKRPLEGGKD 244
OY 249 HVHQIRLTTELTGPTTEADLGLFQONEDAKRYTROLPOHPRQOOLAEFVPVNPALIDLVMK 308
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 245 HVHQRRLTTELTGPTTEADLGLFVRNEDAKRYTROLPRHNRQPLRLQYHPVHLAIDLIDK 304
OY 309 MLTEPPTRTIYVEALDHPYLAKLHDAGDEPICVPVPSFDEFOGIGEOIKDMITYOEAL 368
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 305 MLTEPSPKRITVEEALHPYLAKLHDIDEPICTRKPSFEFEALHGEQIKDMITYOEAL 364
OY 369 SLNPEYA 375
    ||| |
Db 365 AFNPDCA 371

RESULT 5
T09622
C:Species: Medicago sativa (alfalfa)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09622
R:Jonak, C.; Kiegerl, S.; Lighterling, W.; Barker, P.; Huskisson, N.; Hirt, H.
Proc. Natl. Acad. Sci. U.S.A. 93, 11274-11279, 1996
A:Title: Signaling in plants: a mitogen-activated protein kinase pathway is activated by
A:Reference number: 216782; MUID:97008170; PMID:8853346
A:Accession: T09622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-371 <JON>
A:Cross-references: EMBL:X82270; NID:g1667372; PIDN:CA587721.1; PID:g1667373
C:Gene: MKK4
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: phosphotransferase; protein kinase
F:36-325/Domain: protein kinase homology <KIN>

Query Match 82.2%; Score 1634; DB 2; Length 371;
Best Local Similarity 82.8%; Pred. No. 7.7e-72;
Matches 299; Conservative 38; Mismatches 24; Indels 0; Gaps 0;

OY 15 DEPSVLTGHGOYVOPDIFGNFEITTKYRPIMPGRGAYGIVCSVLNTELMENYAVKKI 74
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 11 EPFAVQTHGGQFOYVNGCNLFYVAKYRPIMPGRGAYGIVCSVLNTELMENYAVKKI 70
OY 75 ANAPDIYDAKRTLEIKLRLHDHENYIGLRDVIIPPLRREFSDVYIATELMDTLHQI 134
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 71 ANAFDNHMDAKRTLEIKLRLHDHENYIGLRDVIIPPLRREFSDVYIATELMDTLHQI 130
OY 135 IRSNOGSESDHCQYFMVOLLGKLYHSANYLHRDKPSNLLVYANCDLKITCDGLARP 194
    ||| | :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 131 IRSNONLSDHCQYFLYILGKLYHSANLIHRDKPSNLLVYANCDLKITIDFGLARP 190
OY 195 IENENMTEYVYTRWYRAPPELLNSSDYTAIDVWSVGCIFMELMNKRPLEGGKD 254
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 191 MESDEMTYVYTRWYRAPPELLNSSDYTAIDVWSVGCIFMELMNKRPLEGGKD 250
OY 255 LLETTLGPTTEADLGLFQONEDAKRYTROLPOHPRQOOLAEVPPVNPALIDLVMK 314
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 251 LLETTLGPTTEADLGLFQONEDAKRYTROLPOHPRQOOLAEVPPVNPALIDLVMK 310
OY 315 TRRTIYVEALDHPYLAKLHDAGDEPICVPVPSFDEFOGIGEOIKDMITYOEAL 374
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 311 TRRTIYVEALDHPYLAKLHDAGDEPICVPVPSFDEFOGIGEOIKDMITYOEAL 370
OY 375 A 375
    |
Db 371 A 371

RESULT 6

```

```

S51321
mitogen-activated protein kinase 4 (EC 2.7.1.-) - common tobacco
N:Alternate names: serine/threonine-specific protein kinase p45Ntf4
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 18-Jun-1999
C:Accession: S68190; S51321
R:Wilson, C.; Anglmayer, R.; Vicente, O.; Heberle-Bors, E.
Eur. J. Biochem. 233, 249-257, 1995
A:Title: Molecular cloning, functional expression in Escherichia coli, and characteri
A:Reference number: S68189; MUID:96061956; PMID:7588752
A:Accession: S68190
A:Molecule type: mRNA
A:Residues: 1-393 <WIL>
A:Cross-references: EMBL:X83880; NID:9634069; PIDN:CA58761.1; PID:9634070
C:Gene: ntf4
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:57-345/Domain: protein kinase homology <KIN>
F:66-74/Region: protein kinase ATP-binding motif

Query Match 75.9%; Score 1509; DB 2; Length 393;
Best Local Similarity 72.6%; Pred. No. 7.9e-66;
Matches 278; Conservative 44; Mismatches 49; Indels 12; Gaps 2;

OY 3 DANMGAGGQFP-----DEPSVLTGHGOYVOPDIFGNFEITTKYRPIMPICR 51
    | | | | | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 9 DTVMSDAAQOQAPPSQPVAGIDNIPATLISHGGRFYQYIFGNIFEVYAKYRPIMPICR 68
OY 52 GAYGIVCSVLNTELMENYAVKKIANAFDIYMAKRTLEIKLRLHDHENYIGLRDVIIP 111
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 69 GAYGIVCSVLNTELMENYAVKKIANAFDIYMAKRTLEIKLRLHDHENYIGLRDVIIP 128
OY 112 PLRREPSDVIYATELMDTLHQIIRSNOGSESDHCQYFMVOLLGKLYHSANVLHRDK 171
    | | | | | :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 129 POREAFNDVIYATELMDTLHQIIRSNOGSESDHCQYFMVOLLGKLYHSANVLHRDK 188
OY 172 PSNLLVYANCDLKITCDGLARPNIENENETEVYTRWYRAPPELLNSSDYTAIDVWSV 231
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 189 PSNLLVYANCDLKITCDGLARPNIENENETEVYTRWYRAPPELLNSSDYTAIDVWSV 248
OY 232 CIFMELMNKRPLEGGKD 291
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 249 CIFMELMNKRPLEGGKD 307
OY 292 AEVPPVNPALIDLVMK 351
    ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| ||||| :||| |||||
Db 308 VEKFPVNPALIDLVMK 367
OY 352 QGIGEOIKDMITYOEAL 374
    :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 368 HALTEDEOMKELIYRGGLAFNP 390

RESULT 7
S48123
mitogen-activated protein kinase 7 (EC 2.7.1.-) - alfalfa
N:Alternate names: MAP kinase; MSK7 kinase
C:Species: Medicago sativa (alfalfa)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Jun-1999
C:Accession: S48123; S59949
R:Jonak, C.; Pay, A.; Boegre, L.; Hirt, H.; Heberle-Bors, E.
Plant J. 3, 611-617, 1993
A:Title: The plant homologue of MAP kinase is expressed in a cell cycle-dependent and
A:Reference number: S48123; MUID:94035163; PMID:8220466
A:Accession: S48123
A:Molecule type: mRNA
A:Residues: 1-387 <JON>
A:Cross-references: EMBL:X66469; NID:9298018; PIDN:CA47099.1; PID:9298019
R:Duerr, B.; Gawienowski, M.; Kopp, T.; Jacobs, T.
Plant Cell 5, 87-96, 1993
A:Title: MSERK1: a mitogen-activated protein kinase from a flowering plant.
A:Reference number: S59949; MUID:93177216; PMID:8439746

```


Db 190 LKPSNLLNANCDLKICDGLARVTSSESDFMTEYVTRWYRAPPELLNNSDYTAIDVMS 249
QY 230 VCCIFEMELNKRKPLFGCKDGHVHDIRLTLLGTPTEADIGFLQNEADAKRYIRQLPOHPRO 289
Db 250 VCGIFELMDKRPDLFGKHVHQLRLMELIGPSESEELFL-NEAKKRIQLPPYPO 308
QY 290 QLAIEVPHVPLAIDLVDMDLTFDPTRITVEALDHPYLAIKLHDAGDPICVPSPFP 349
Db 309 SITDKRPYVHPLAIDLIELMLTFDPRRRTIVDALAHPLNLSLHDSDEPCTIRPNPDE 368
QY 350 EEOGIGEEQIKDIIYOALSINPEY 374
Db 369 ENHALSEOMKELIYREALAFNPEY 393

RESULT 10

S56638
mitogen-activated protein kinase 1 homolog (clone AspK9) - oat
N:Alternate names: MAP1 kinase
C:Species: Avena sativa (oat)
C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 18-Jun-1999
C:Accession: S56638
R:Huttlly, A.K.; Phillips, A.L.
Plant Mol. Biol. 27, 1043-1052, 1995
A>Title: Gibberellin-regulated expression in oat aleurone cells of two kinases that show
A:Reference number: S56638; MUID:95284341; PMID:7766874
A:Accession: S56638
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-369 <HUT>
A:Cross-references: EMBL:X79993; NID:g871983; PIDN:CA56314.1; PID:g871984
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; protein kinase
F:33-322/Domain: protein kinase homology <KIN>
F:42-50/Region: protein kinase ATP-binding motif

Query Match 74.1%; Score 1473; DB 2; Length 369;
Best Local Similarity 72.9%; Pred. No. 4e-64;
Matches 266; Conservative 52; Mismatches 47; Indels 0; Gaps 0;

QY 10 GGOFDPFVYLTHGGQYVDFIFGNFETITTKYRPPIMPICGAYICVSLNTELEMY 69
Db 3 GAPVAEFRTMGGREFLLYNIFGNQFELTSKYQRPIMPICGAYICVSNMFTREMY 62
QY 70 AKKIANAFDIYMDAKRTLRREIKLRLHLDHENYIGLRDVIYPPRLREFSDVYATLMDT 129
Db 63 AKKIANAFDIYMDAKRTLRREIKLRLHLDHENYIGLRDVIYPPRLREFSDVYATLMDT 122
QY 130 DLHQIIRSNQGLSEDHCOYMTQLRGKLYHSANVLRDLKPSNLLVANCDLKICDGL 189
Db 123 DLHIIIRSNQGLSEDHCOYMTQLRGKLYHSANVLRDLKPSNLLVANCDLKICDGL 182
QY 190 LARPNIENMTYVTRRYRAPPELLNNSDYTAIDVMSVGCIFEMELNKRKPLFGCKDH 249
Db 183 LARPSESDMTEYVTRRYRAPPELLNNSDYTAIDVMSVGCIFEMELNKRKPLFGCKDH 242
QY 250 VHQIRLTLELTGTEADIGFLQNEADAKRYIRQLPOHPQOLAIEVPHVPLAIDLVDMA 309
Db 243 MHQMRITIVETGTPDDDLGFIINDEAKRYKMLRQFRPRRPPGCKYQAPALDIERK 302
QY 310 LTFDPTRITVEALDHPYLAIKLHDAGDPICVPSPFDEOOGIGEEQIKDIIYOALS 369
Db 303 LTFNPLQRTIVEALEHRYLERLHVADBERICTDPFSFDEQHPRLTEDQMKOILFEALE 362
QY 370 LNPEY 374
Db 363 LNPNE 367

RESULT 11

S40470
mitogen-activated protein kinase 4 (BC 2.7.1.-) - Arabidopsis thaliana
N:Alternate names: MAP kinase

C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 06-Oct-1994 #sequence_revision 19-Jan-1996 #text_change 03-May-2002
C:Accession: S40470 #sequence_revision 19-Jan-1996 #text_change 03-May-2002
R:Minoguchi, T.; Hayashida, N.; Yamaguchi-Shinozaki, K.; Kamada, H.; Shinozaki, K.
FEBS Lett. 336, 440-444, 1993
A>Title: ATPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.
A:Reference number: S40469; MUID:94109583; PMID:8282107
A:Accession: S40470
A:Molecule type: mRNA

A:Residues: 1-376 <MIN>
A:Cross-references: EMBL:D21840; NID:g457399; PIDN:BAA04867.1; PID:g457400
R:Schmitt, P.; Magg, L.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of A. thaliana IG002N01.
A:Reference number: 214407
A:Accession: T01707
A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA
A:Residues: 1-40, 'N', '59-147, 153-312, 'D', 314-376 <SCH>
A:Cross-references: EMBL:AF007269; NID:g2191126; PIDN:AMB61033.1; PID:g2191146

R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A>Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: AB5001; MUID:20083488; PMID:10617198
A:Accession: H85017
A>Status: preliminary

A:Molecule type: DNA
A:Residues: 1-312, 'D', 314-376 <STO>
A:Cross-references: GB:NC_001268; NID:g7267634; PIDN:CAB80946.1; GSPDB:GN00140

C:Genetics:
A:Gene: MPK4; AT4g01370
A:Map position: 4
A:introns: 41/2; 101/3; 147/3; 258/3; 320/1
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:40-329/Domain: protein kinase homology <KIN>
F:49-57/Region: protein kinase ATP-binding motif

Query Match 67.5%; Score 1340.5; DB 2; Length 376;
Best Local Similarity 65.1%; Pred. No. 8.9e-58;
Matches 242; Conservative 64; Mismatches 65; Indels 1; Gaps 1;

QY 2 ADANMGAGGQPPFVYLTHGGQYVDFIFGNFETITTKYRPPIMPICGAYICVSL 61
Db 3 AASCFFSSDDQ-SSSKGVAATHGSSQYQVYVGNLFVSKYPPPLKICGAYICATF 61
QY 62 NTELNMAVAVKTIANAFDIYMDAKRTLRREIKLRLHLDHENYIGLRDVIYPPRLREFSDVY 121
Db 62 NSETGEVAIKKIGNAFDNIIDAKRTLRREIKLRLHLDHENYIAVKDIIRPPQENENDVY 121
QY 122 IATELMDTDLHQIIRSNQGLSEDHCOYMTQLRGKLYHSANVLRDLKPSNLLVANNC 181
Db 122 IYTELMDTDLHQIIRSNQGLSEDHCOYMTQLRGKLYHSANVLRDLKPSNLLVANNC 181
QY 182 DLKICDGLARPNIENMTYVTRRYRAPPELLNNSDYTAIDVMSVGCIFEMELNKR 241
Db 182 DLKIDGFLGARPNIENMTYVTRRYRAPPELLNNSDYTAIDVMSVGCIFEMELNKR 241
QY 242 PLFPGKDVHQLRLTELGTPEADIGFLQNEADAKRYIRQLPOHPQOLAIEVPHVPL 301
Db 242 PLFPGKDVHQLRLTELGTPEADIGFLQNEADAKRYIRQLPOHPQOLAIEVPHVPL 301
QY 302 AIDLVDKMLTFDPTRITVEALDHPYLAIKLHDAGDPICVPSPFDEOOGIGEEQIKD 361
Db 302 AVDLEKMLVPEPSRRIIVDEALCHPLAIDLHINEEPCVPRPNDPFOPTLEENIKE 361
QY 362 MIYOALSINPE 373
Db 362 LIYRETVKFNPO 373

RESULT 12

S60121

Db 129 QTLTDHCOYFLYQILRGKIYHSANVLHRDLKPSNLVLTNDLKIICDFGLARTSNETE 188
QY 199 NMTEVYVFWYRAPPELLNSSDYTAIDWWSGCI FMEIMNRKPLFGCKDHQIRLLPE 258
Db 189 IMTEVYVFWYRAPPELLNSSDYTAIDWWSGCI FMEILRRETLFPKGYVOQLKITE 248
QY 259 LIGTTEADLGFIONEDAKRYIRQLPQHROQLAEVFPVNPPLAIDLVDKMLTFDPTRRI 318
Db 249 LIGSPDSDSLDPLRSDNARKYKQLPHVOKOSFREKFPNISPALDLAKMLVFPDSKRI 308
QY 319 TVEEALDHPYLAKLHDAGDEPICVPVPSFPEQOGIGEBQIKDMITYQAL 368
Db 309 TVDEALKQYLAHLSEINEPTCPPEFSPFETALDEQDIKELVWRESL 358

RESULT 15

T47803
mitogen-activated protein kinase-like protein - Arabidopsis thaliana
N:Alternate names: protein F24G16.60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47803
R:D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, February 2000
A:Reference number: 224477
A:Accession: T47803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <DAN>
A:Cross-references: EMBL:AL138647
A:Experimental source: cultivar Columbia; BAC clone F24G16
C:Genetics:
A:Map position: 3
A:Introns: 75/2; 118/3; 164/3; 275/3; 336/1
A:Note: F24G16.60
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 64.4%; Score 1279.5; DB 2; Length 393;
Best local Similarity 66.3%; Pred. No. 7.8e-55;

Matches 238; Conservative 51; Mismatches 69; Indels 1; Gaps 1;

QY 15 DPPSVLTGGQYVQDFDIFGNFETTKYRPIPIPIGAGYGVSVLNTLNMVAVKKI 74
Db 32 DIPGTLSDHGRYIQYNLFCHIFELPAKYKPIPIPIGAGYGVSVLNTLNMVAVKKI 91
QY 75 ANAPDIYMDAKRTLRLEIKLRHLDBENVIGLRDVIIPPLRREPSDVIYATLMDTDLHOI 134
Db 92 TQVFNPTLEAKRTLRLEIKLRHLDBENVIVAIRDVIILPQDSFEDVIYVNEIMLEFIDLRT 151
QY 135 IRSNGLSSEDHGQYFMYQLLRGLKTYHSANVLHRDLKPSNLVLTNDLKIICDFGLARP 194
Db 152 LKSDDELTKDHGMFYQLLRGLKTYHSANVLHRDLKPSNLVLTNDLKIICDFGLARP 211
QY 195 IENENMTEVYVFWYRAPPELLNSSDYTAIDWWSGCI FMEIMNRKPLFGCKDHQIR 254
Db 212 PESNLMTEVYVFWYRAPPELLNSSDYTAIDWWSGCI FMEIMNRKPLFGCKDHQIR 271
QY 255 LTELIGTTEADLGFIONEDAKRYIRQLPQHROQLAEVFPVNPPLAIDLVDKMLTFDP 314
Db 272 LTELIGTTEADLGFIONEDAKRYIRQLPQHROQLAEVFPVNPPLAIDLVDKMLTFDP 330
QY 315 TRRITVEEALDHPYLAKLHDAGDEPICVPVPSFPEQOGIGEBQIKDMITYQALSLNPE 373
Db 331 KORISVKEALAHPLVLSFHDITDEPCSEPFNLDLDEHPFSEQFRELITYCEALAFNPE 389

Search completed: May 20, 2003, 00:24:29
Job time : 44 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 19, 2003, 23:01:26 ; Search time 37 Seconds

(without alignments)
420.368 Million cell updates/sec

Title: US-09-623-034-2

Perfect score: 1987
Sequence: 1 MADANGAGCGGFPDPFVS.....EEOIKDMTQELSLNPEYA 375

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	83.6	370	1	MPK3_ARATH
2	1509	75.9	393	1	Q40532 arabidopsi
3	1500.5	75.5	387	1	Q00176 medicago sa
4	1498.5	75.4	394	1	Q06060 pisum sativ
5	1498.5	75.4	395	1	Q39026 arabidopsi
6	1344.5	67.7	376	1	Q39024 arabidopsi
7	1312	66.0	371	1	Q40353 medicago sa
8	1292	65.0	371	1	Q40531 arabidopsi
9	1284	64.6	376	1	Q39025 arabidopsi
10	1094.5	55.1	372	1	Q40517 arabidopsi
11	1078	54.3	370	1	Q39021 arabidopsi
12	1075.5	54.1	384	1	Q40884 petunia hyb
13	1069	53.8	376	1	Q39022 arabidopsi
14	1061	53.4	368	1	Q39027 arabidopsi
15	1038.5	52.3	415	1	P42525 dictyosteli
16	896.5	45.1	444	1	P39745 caenorhabdi
17	883	44.4	380	1	P21708 rat mitogen-a
18	878.5	44.2	360	1	P28482 homo sapien
19	878	44.2	806	1	Q94988 mus musculu
20	878	44.2	815	1	Q13164 homo sapien
21	877.5	44.2	358	1	P27703 mus musculu
22	877.5	44.2	360	1	P61696 bos taurus
23	877.5	44.2	361	1	P26696 xenopus lae
24	875	44.0	349	1	O09892 schizosacch
25	872	43.9	372	1	P27638 schizosacch
26	872	43.9	379	1	P27361 h mitogen-a
27	868	43.7	353	1	P16892 saccharomyc
28	868	43.5	365	1	P22485 saccharomyc
29	864.5	43.4	376	1	O61417 drosophila
30	862.5	43.0	417	1	P40417 drosophila
31	854	42.8	366	1	P28866 candida alb
32	850.5	42.6	361	1	O62618 drosophila
33	846	42.6	361	1	Q90336 cypripus ca

34	845.5	42.6	377	1	HOG1_CANAL
35	841	42.3	360	1	MPK14_MOUSE
36	839	42.2	360	1	MPK14_RAT
37	838	42.2	360	1	MPK14_HUMAN
38	837	42.1	422	1	SPM1_SCHPO
39	836	42.1	360	1	MPK14_CANPA
40	831.5	41.8	314	1	MPK03_MOUSE
41	830	41.8	361	1	MPK14_XENIA
42	828.5	41.7	484	1	SLT2_YEAST
43	824	41.5	501	1	MPK1_CANAL
44	807.5	40.6	364	1	MPK1_MOUSE
45	806.5	40.6	372	1	MPK1_HUMAN

ALIGNMENTS

RESULT 1

ID	MPK3_ARATH	STANDARD:	PRT:	370 AA.
AC	Q39023: Q9M1E3:			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Mitogen-activated protein kinase homolog 3 (EC 2.7.1.-) (MAP kinase 3)			
DE	(AEMPK3).			
GN	MPK3 OR AT3G45640 OR FPK21.220 OR T6D9.4.			
OS	Arabidopsis thaliana (mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eurosid; II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	MEDLINE=94109583; PubMed=8282107;			
RA	Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,			
RI	"RIMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana."			
RL	FEBS Lett. 336:440-444(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RA	MEDLINE=21016720; PubMed=11130713;			
RA	Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unsel M.,			
RA	Fatmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,			
RA	De Simone V., Boutry M., Griwell L.A., Maché R., Puigdomenech P.,			
RA	De Simone V., Choisme N., Artiguenave F., Robert C., Brotlier P.,			
RA	Wincker P., Catalicio L., Weissenbach J., Saurin W., Quetier F.,			
RA	Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,			
RA	Wummbach E., Dronek H., Effie H., Jordan N., Bangert S.,			
RA	Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nykatura G.,			
RA	Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,			
RA	Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,			
RA	Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,			
RA	Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchenin D.,			
RA	Cooke R., Landie M., Berger-Liauro C., Purrelle B., Masny D.,			
RA	de Haan M., Maestre A.C., Alcaraz J.-P., Cottet A., Casacubeta E.,			
RA	Monfort A., Argirion A., Flores M., Liguori R., Vitale D.,			
RA	Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,			
RA	Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,			
RA	Rooney T., Rizzo M., Wals A., Uterback T., Fujii C.Y., Shea T.P.,			
RA	Crosby T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,			
RA	Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,			
RA	Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,			
RA	Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,			
RA	Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,			
RA	Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,			
RA	Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,			
RA	Watanabe A., Yamada M., Yasuda M., Tabata S.,			
RT	"Sequence and analysis of chromosome 3 of the plant Arabidopsis			
RT	thaliana."			
RL	Nature 408:820-822(2000).			

```

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Piker Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT SSP consortium (Salk/Stanford/PGSC).";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D21839; BAA04866.1; -
DR EMBL; AL138657; CAB75493.1; -
DR EMBL; AL157735; -; NOT_ANNOTATED_CDS.
DR EMBL; AF386961; AAK62406.1; -
DR HSSP; Q16539; IMPC.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MARK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation: Multigene family.
FT DOMAIN 38 324 PROTEIN KINASE.
FT NP_BIND 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT MOD_RES 196 196 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 198 198 (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT CONFLICT 15 15 E -> D (IN REF. 1).
FT SEQUENCE 370 AA; 42716 MW; 6992A7D97FC9841 CRC64;
SQ
Query Match 83.6%; Score 1662; DB 1; Length 370;
Best Local Similarity 82.4%; Pred. No. 2.2e-101;
Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

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Db 301 VDRMLTFDPNRRITVEQALNHQYLAKLHDPNDEPICQPFSEFEQOPLDEQIKEMIQ 360
OY 366 EALSLNPEX 374
Db 361 EALINLPTV 369
RESULT 2
NTF4_TOBAC STANDARD; PRT; 393 AA.
ID NTF4_TOBAC
AC Q40532;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF4 (EC 2.7.1.-) (P45).
GN NTF4.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OC NCBI_Taxid=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-cv. Petite Havana SRL;
RX MEDLINE=96061956; Pubmed=7586752.
RA Wilson C., Anglmayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco";
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL; X83880; CAA58761.1; -
DR HSSP; P27703; IERK.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR003527; MAP_kin.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS01351; MARK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation: Multigene family.
FT DOMAIN 60 345 PROTEIN KINASE.
FT NP_BIND 66 74 ATP (BY SIMILARITY).
FT BINDING 89 89 ATP (BY SIMILARITY).
FT ACT_SITE 186 186 BY SIMILARITY.
FT MOD_RES 218 218 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 220 220 (BY SIMILARITY).
FT MOD_RES 220 220 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT SEQUENCE 393 AA; 45119 MW; 76EC1F3B1F174AB9 CRC64;
SQ
Query Match 75.9%; Score 1509; DB 1; Length 393;
Best Local Similarity 72.6%; Pred. No. 2.1e-91;
Matches 278; Conservative 44; Mismatches 49; Indels 12; Gaps 2;

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OY 3 DANMAGGGGPP-----DPPSVLTHGGOVQVOPDINGNFFETITTKRPPIMPICR 51
DB 9 DTVMSDAAGQOPAPPSPQVAGIDNIPATLSHGGRFIQYVIFGNIFEVYAKYKPPIMPICG 68
OY 52 GAYGVCSVLNTELEMEVAVKKIANAFDIYMDAKRTLEIKRLRLHDEHNYGLRDVIPP 111
DB 69 GAYGVCSALNSETNEHVAIKKIANAFDNKIDAKRTLEIKRLRLHDEHNYAIRDIIPP 128
OY 112 PLRREPSDVYIATLMDTDLHQIIRSNQGLSEDCQYEMYOLLRLGLKYHSANVLRDLK 171
DB 129 FQREAFNBYIYATLMDTDLHQIIRSNQGLSEHCQYFLYQLRLGLKYHSANVLRDLK 188
OY 172 PSNLLVYANNCIDKICDFGLARPNINENMTEVYVTRWRAPPELLNSSDYTAIDVWSVG 231
DB 189 PSNLLVYANNCIDKICDFGLARPNINENMTEVYVTRWRAPPELLNSSDYTAIDVWSVG 248
OY 232 CIFNELMNRKPLFGGKDHVQIRLTELIGTPTTEADLGLQNEADKRYRQLPQHRQOL 291
DB 249 CIFNELMNRKPLFGGKDHVQIRLTELIGTPTTEADLGLQNEADKRYRQLPQHRQOL 307
OY 292 AEVPHVNPALIDVVKMLTFDPTRRTIVEEALDHPYLAKLHDAGDEPICVPFSFDEQ 351
DB 308 VEKPHVNPALIDVVKMLTFDPTRRTIVEEALDHPYLAKLHDAGDEPICVPFSFDEQ 367
OY 352 OGIGEOIKDMYOFALSINPEY 374
DB 368 HALTEOMKELIYREGIAFNPEY 390

RESULT 3
MKK1_MEDSA
ID MKK1_MEDSA STANDARD: PRT: 387 AA.
AC Q07176;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog MKK1 (EC 2.7.1.-) (MAP kinase
DE MSK7) (MAP kinase ERK1).
CN MKK1 OR MSK7 OR ERK1.
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
OY NCBI_TaxID=3879;
RX SEQUENCE FROM N.A.
RP TISSUE=Embryo;
RC TISSUE=Embryo;
RA Jonak C., Pay A., Boegre L., Hirt H., Heberle-Bors E.;
RT "The plant homologue of MAP kinase is expressed in a cell cycle-
RT dependent and organ-specific manner.";
RL Plant J. 3:611-617(1993).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Iroquois; TISSUE=Seedling root;
RC MEDLINE=93177216; PubMed=8439746;
RA Duert B., Gawienowski M., Ropp T., Jacobs T.;
RT "MSK1: a mitogen-activated protein kinase from a flowering plant.";
RL Plant Cell 5:87-96(1993).
CC -1- FUNCTION: MAY PLAY A ROLE IN THE MITOGENIC INDUCTION OF SYMBIOTIC
CC ROOT NODULES ON ALFALFA BY RHIZOBIUM SIGNAL MOLECULES.
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: ROOTS AND STEMS.
CC -1- PTM: AUTOPHOSPHORYLATED.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC DR EMBL: X66469; CAA47099.1; -.
CC DR EMBL: L07042; AAB41548.1; -.
CC HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF000069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MARK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; serine/threonine-protein kinase; ATP-binding;
KW Mitosis; Cell cycle; Conjugation; Phosphorylation.
KW DOMAIN
FT NP_BIND 61 69 ATP (BY SIMILARITY).
FT BINDING 84 84 ATP (BY SIMILARITY).
FT ACT_SITE 181 181 BY SIMILARITY.
FT MOD_RES 213 213 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
FT MOD_RES 215 215 PHOSPHORYLATION (ACTIVATES THE KINASE).
SQ SEQUENCE 387 AA; 44401 MW; 8672871A5D34EAD2 CRC64;

Query Match 75.5%; Score 1500.5; DB 1; Length 387;
Best Local Similarity 74.3%; Pred. No. 7.3e-91;
Matches 278; Conservative 43; Mismatches 52; Indels 1; Gaps 1;

OY 1 MADANMAGGGGPPDPSPSVLTHGGOVQVOPDINGNFFETITTKRPPIMPICRGAYGVCSV 60
DB 13 MDDAAPAPPOMKIEINIPAVLSHGGRFIQYVIFGNIFEVYAKYKPPIMPICRGAYGVCSA 72
OY 61 LMTLEMEVAVKKIANAFDIYMDAKRTLEIKRLRLHDEHNYGLRDVIPPPLRREFSDV 120
DB 73 HNSETEHVAVKKIANAFDNKIDAKRTLEIKRLRLHDEHNYAIRDIIPPQREAFNDV 132
OY 121 YATLEMDTDLHQIIRSNQGLSEDCQYEMYOLLRLGLKYHSANVLRDLKPSNLLVYAN 180
DB 133 YATLEMDTDLHQIIRSNQGLSEHCQYFLYQLRLGLKYHSANVLRDLKPSNLLVYAN 192
OY 181 CDLKTCDPGLARPNINENMTEVYVTRWRAPPELLNSSDYTAIDVWSVGCIFMELMDR 240
DB 193 CDLKTCDPGLARPNINENMTEVYVTRWRAPPELLNSSDYTAIDVWSVGCIFMELMDR 252
OY 241 KPLFGKDHVQIRLTELIGTPTTEADLGLQNEADKRYRQLPQHRQOLAEVPHVNP 300
DB 253 KPLFGKDHVQIRLTELIGTPTTEADLGLQNEADKRYRQLPQHRQOLFQEKFPVHNP 311
OY 301 LAIDLVDKMLTFDPTRRTIVEEALDHPYLAKLHDAGDEPICVPFSFDEQOGIGEOIK 360
DB 312 EAIDLVEKMLTFDPTRRTIVEEALDHPYLAKLHDAGDEPICVPFSFDEQHALTEOMK 371
OY 361 DMATYOFALSINPEY 374
DB 372 ELIYREGIAFNPEY 385

RESULT 4
MARK_PEA
ID MARK_PEA STANDARD: PRT: 394 AA.
AC Q06060;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog D5 (EC 2.7.1.-).
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.

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KM Phosphorylation: Multigene family.
 FT DOMAIN 63 348 PROTEIN KINASE.
 FT NE_BIND 69 77 ATP (BY SIMILARITY).
 FT BINDING 92 92 ATP (BY SIMILARITY).
 FT ACT_SITE 189 189 BY SIMILARITY.
 FT MOD_RES 221 221 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT (BY SIMILARITY).
 FT MOD_RES 223 223 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT (BY SIMILARITY).
 SQ SEQUENCE 395 AA; 45057 MW; 296D2BD753C6DD44 CRC64;
 Query Match 75.4%; Score 1498.5; DB 1; Length 395;
 Best Local Similarity 71.4%; Pred. No. 1e-90;
 Matches 275; Conservative 49; Mismatches 48; Indels 13; Gaps 2;
 QY 2 ADANMGAGGQFP-----DPPSVLTGGQYVQDPFGNFEITTKYPPIMPI 49
 DB 10 ADTEMTAPGFFPAAPSPQMPGIENTPATLSHGCRFQYMFQNIPEVTAKYKPIMPI 69
 QY 50 GRGAYGVCSVLTENLNMVAVKRIANAFDYMDAKRFLRKLRHLDHENVGLRDVI 109
 DB 70 GKRGAYGVCSAMNSETESVAIKRIANAFDNKIDAKRFLRKLRHLDHENVGLRDVI 129
 QY 110 PPLRLREFSDVYIATLMDTDLHQIIRSNQSLSEDCQYEMVQQLRGLKTHSANVLRHD 169
 DB 130 PPLRLNMFNDYIAYELMDTDLHQIIRSNQSLSEDCQYFLYQLRGLKTHSANVLRHD 189
 QY 170 LKPSNLLVANNCDLKIDCGFLARPNINENNTVEVYTRWYAPPELLNSSDYTAIDWMS 229
 DB 190 LKPSNLLVANNCDLKIDCGFLARPNINENNTVEVYTRWYAPPELLNSSDYTAIDWMS 249
 QY 230 VGCIFMELMNRKPLFGSKDHYHQIRLTLLTGTPTEADLGFQMDKARYRQLPQHPRO 289
 DB 250 VGCIFMELMNRKPLFGSKDHYHQIRLTLLTGTPTEADLGFQMDKARYRQLPQHPRO 308
 QY 290 QLAEEFVHVNPPLAIDVYDKMTFDPTRRTIYEALDHPYLAKLHDAGDEPICVPFSEDF 349
 DB 309 SLDKFEPTVPLAIDLIEKMTLPDRRRITVIALAPHYLSLHDIDSEPECTIPFNFDF 368
 QY 350 EEOGIGEEQIKDMTQYQALSLNPEY 374
 DB 369 ENHALSEQMKELITREALAFNPEY 393
 RESULT 6
 MPK4 ARATH STANDARD; PRT; 376 AA.
 ID MPK4.ARATH 09M136; 004597;
 AC Q39024; 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase homolog 4 (EC 2.7.1.-) (MAP kinase 4)
 DE (AtMPK4).
 GN MPK4 OR ATG601370 OR F2N1.1 OR F2N1-2-t.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94109583; PubMed=8282107;
 RA Shinozaki K., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RT "ATMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana";
 RL FEBS Lett. 336:440-444(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=2008348; PubMed=10617198;
 RA Mayer K.F.X., Schaefer C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,

RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Deiseny M., Puigdomenech P., Watson M., Schmidtmann T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hobeisel J., Zimmermann W., Wedler H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schuren J., Grymonprez B., Chiang Y.-J., Vandenbussche F.,
 RA Braeken M., Weljens I., Voet M., Bastlaens U., Aert R., Defoor E.,
 RA Weitzengger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirkse W.,
 RA Moolman P., Klein Lankhorst R., Rose M., Hauf J., Koester P.,
 RA Benneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
 RA De Keyser A., Buyshaert C., Gijlen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
 RA Petlet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Lohmert T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner D., Herzl A.,
 RA Neumann S., Argüello A., Vitale D., Liguori R., Pivrandi E.,
 RA Massenet O., Quigley F., Clabaud G., Muenlein A., Felber R.,
 RA Schindl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Cleofor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
 RA Glibons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bielke C.,
 RA Frishman D., Haase D., Lemcke K., Meyes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Pannell L., Dedhia N., Gnoj L., Schütz K., Huang E., Spiegel L.,
 RA Sakhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
 RA Stoneking T., Kalicki J., Graves T., Harwood G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Pulton L., Mardis E., Dante M., Pegin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
 RA Antonolli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vil D., Shekhar M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
 RA Granat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Tili S.,
 RA Chen E., Marra M., Martienssen R., McCombe W.R.,
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 thaliana";
 RL Nature 402:769-777(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,
 RT "Riken Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THRONINE
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -1- CAUTION: Ref. 2 (AA061033) sequence differs from that shown due
 CC to erroneous gene model prediction.
 CC
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 CC
 CC EMBL: D21840; BAB04867.1; -;
 CC EMBL: AL161491; CAB80946.1; -;
 CC EMBL: AF007269; AAB61033.1; ALT_SEQ.
 CC EMBL: AF360231; AAK25941.1; -;
 CC EMBL: AY040031; AAK64089.1; -;
 CC HSSP: Q16539; IWFC.
 CC InterPro: IPR000719; Euk_pkinase.


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ID NTF6_TOBAC STANDARD: PRT: 371 AA.
AC Q40531.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF6 (EC 2.7.1.-) (P43).
GN NTF6.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
ON NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=96061956; PubMed=7588752;
RA Wilson C., Anglimayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco."
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: X83879; CAAS8760.1; -
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_Kin.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR Pfam: PF00068; Pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 38 324 PROTEIN KINASE.
FT NP_BIND 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT MOD_RES 196 196 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
FT MOD_RES 198 198 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT (BY SIMILARITY).
SQ SEQUENCE 371 AA; 42741 MW; 4D97C41AC203C272 CRC64;
Query Match 65.0%; Score 1292; DB 1; Length 371;
Best Local Similarity 62.8%; Pred. No. 2.5e-77;
Matches 225; Conservative 70; Mismatches 63; Indels 0; Gaps 0;
OY 15 DFFSVLTHGGOYVDFDGNFFELTKRPPIMPGRAVIGSVLTLEMLNEMVAVKI 74
DB 10 EIKIPHEGKYVEYNVLGNFEVTSKIPPIOPVGRGAYMCCATSEKKEEVAIKKI 69
OY 75 ANADIYADAKRTREIKLRLHLENYIGRVPLPLREDFSPVYATLEMDLHIOI 134
DB 70 GNAEFENRKARTRLEIKLLSHMDHENIKIKNDIYRPDPREFNDVYIVTELMDLHIOI 129
OY 135 IRSNOGLSEDHCOYFMVQLLGLAYIHSANVJLHRLDKPSNLLVANCDLKCIDGLARP 194

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DB 130 IRSSQALTDHHCQYFLYQLLGLKAYVHSANVJLHRLKPSNLLVANCDLKCIDGLARP 189
OY 195 IENENMTEYVTRWYRAPPELLNSDYTAIDWVSGCITEMLNKRPLFGKDHVHOIR 254
DB 190 SEADFMTEYVTRWYRAPPELLNCTEYTAIDWVSGCITEMLNKRPLFGKDHVHOIR 249
OY 255 LTLELGTPTADTGFELONEDAKRYIRQLPQROQLAEVPHVPLAIDLVDKLTEDP 314
DB 250 LTALLGSPEDSDGLFSLSDNARKVKHLPVPRHPSQKPEPDSPLDLAERMLVFP 309
OY 315 TRRTVEEALDHPYLAUKLDAGDEPICVPFSFDFEQOIGEEQIKDVIYOEALSLNP 372
DB 310 AKRIVEDALNHPFLISLHEINEEPVCSDFNEDEQASLSDDOIKELINNEALKFDP 367
RESULT 9
MPK5_ARATH STANDARD: PRT: 376 AA.
AC Q39025; Q9SUS8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase homolog 5 (EC 2.7.1.-) (MAP kinase 5)
DE (AtMPK5).
GN MPK5 OR AT4G11330 OR FBL21.120.
OC Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustersoids II; Brassicales; Brassicaceae; Arabidopsis.
ON NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=94109583; PubMed=8282107;
RA Mizoguchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
RA Shinozaki K.;
RT "ATMPK5: a gene family of plant MAP kinases in Arabidopsis thaliana."
RL FEBS Lett. 336:440-444(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Anstorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohenseil J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Gymnopoulos B., Chung Y.-J., Vandenbussche F.,
RA Breken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., van Stevenen M., Dikse M.,
RA Moolman P., Klein lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernerster S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA de Keyser A., buysschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail A., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIay K., Mayes R.,
RA Petteit A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA Botkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Mearse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fatmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argitlon A., Vitale D., Liguori R., Piravandi E.,
RA Massenot O., Quigley F., Clabaud G., Wuendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Cheifod F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bleke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,

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RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stenking T., Kallio J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Min P., Bentley D., Fulton L., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Speth J., Ryan E., Andrews S., Gelsel C., Layman D.,
RA Du H., All J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Grady I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shondy N., Hasegawa A., Hameed A., Lochi M., Johnson A.,
RA Chen E., Maria M., Matlenssen R., McCombie W.R.,
RT Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana." ;
RL Nature 402:769-777(1999).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- CAUTION: Ref.2 sequences differ from that shown due to erroneous
CC gene model prediction.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D21841; BAA04868.1; .
DR EMBL: AL096882; CAB51417.1; ALT_SEQ.
DR EMBL: AL165531; CAB81234.1; ALT_SEQ.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
KW Transfease; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
FT DOMAIN 43 329 PROTEIN KINASE.
FT NP_BIND 49 57 ATP (BY SIMILARITY).
FT BINDING 72 72 ATP (BY SIMILARITY).
FT ACT_SITE 169 169 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 201 201 (BY SIMILARITY).
FT MOD_RES 203 203 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 203 203 (BY SIMILARITY).
FT CONFLICT 59 59 A->P (IN REF. 1).
FT CONFLICT 276 277 AR->GG (IN REF. 1).
SQ SEQUENCE 376 AA; 43207 MW; 2E8C0E5FC47685DF CRC64;
Query Match 64.6%; Score 1284; DB 1; Length 376;
Best Local Similarity 65.0%; Pred. No. 8.4e-77;
Matches 220; Conservative 62; Mismatches 62; Indels 0; Gaps 0;
OY 19 VLTGGQYVDFEGNFEFTTKYRPPIMPDIGAGYGVSVNTELTENAVAKKINAF 78
DB 19 VLTGGQYVDFEGNFEFTTKYRPPIMPDIGAGYGVSVNTELTENAVAKKINAF 78
OY 79 DIYMAKRTRETKLRLHLDHENVIGIRVDYIPPLLRRESVDYIATLMDTDJHQIIRSN 138
DB 79 DIYMAKRTRETKLRLHLDHENVIGIRVDYIPPLLRRESVDYIATLMDTDJHQIIRSN 138
OY 79 DNVDAKRTRETKLRLHLDHENVIGIRVDYIPPLLRRESVDYIATLMDTDJHQIIRSN 138
DB 79 DNVDAKRTRETKLRLHLDHENVIGIRVDYIPPLLRRESVDYIATLMDTDJHQIIRSN 138
OY 139 QGISPDHCQYFMQGLRGKLYHSANVLRHDLKPSNLTVANANDKICDGLARPNTENE 198
DB 139 QGISPDHCQYFMQGLRGKLYHSANVLRHDLKPSNLTVANANDKICDGLARPNTENE 198

DB 139 QGISPDHCQYFMQGLRGKLYHSANVLRHDLKPSNLTVANANDKICDGLARPNTENE 198
OY 199 NMEYVYTRVYRAPPELLINSDDTYAIDVMSVGCIFEMELNRRKPLFCGRDHYQIRLLTE 258
DB 199 NMEYVYTRVYRAPPELLINSDDTYAIDVMSVGCIFEMELNRRKPLFCGRDHYQIRLLTE 258
OY 259 LIGTPTEADIGFLONEDAKRYIRQLPQHPROOLAEPVPHVNPALDLDVMDLTFDPTRTI 318
DB 259 LIGTPTEADIGFLONEDAKRYIRQLPQHPROOLAEPVPHVNPALDLDVMDLTFDPTRTI 318
OY 319 TVEALDHPRLALHAGDEPICVPSPFDEQIGDEIKIMIVQALSLMP 372
DB 319 TVEALDHPRLALHAGDEPICVPSPFDEQIGDEIKIMIVQALSLMP 372
OY 319 TVEALDHPRLALHAGDEPICVPSPFDEQIGDEIKIMIVQALSLMP 372
DB 319 TVEALDHPRLALHAGDEPICVPSPFDEQIGDEIKIMIVQALSLMP 372
RESULT 10
ID NTF3_TOBAC STANDARD; PRT; 372 AA.
AC Q40517;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog NTF3 (EC 2.7.1.-) (P43).
GN NTF3.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=94033334; PubMed=8219089;
RA Wilson C., Eller N., Gartner A., Vicente O., Heberle-Bors E.;
RT "Isolation and characterization of a tobacco cDNA clone encoding a
RT putative MAP kinase";
RL Plant Mol. Biol. 23:543-551(1993).
RN [2]
RP MOTAGENESIS.
RC STRAIN=cv. Petit Havana SRI;
RX MEDLINE=96061956; PubMed=7588752;
RA Wilson C., Anglmayer R., Vicente O., Heberle-Bors E.;
RT "Molecular cloning, functional expression in Escherichia coli, and
RT characterization of multiple mitogen-activated-protein kinases from
RT tobacco";
RL Eur. J. Biochem. 233:249-257(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: UBIQUITOUS.
CC -1- DEVELOPMENTAL STAGE: DETECTED DURING GAMETOPHYTIC POLLEN
CC DEVELOPMENT AND CONSTITUTIVELY EXPRESSED IN EMBRYOGENIC POLLEN.
CC -1- PTM: VERY LOW AUTOPHOSPHORYLATION, ALTHOUGH DRAMATICALLY INCREASED
CC WHEN MN2+ IS ADDED TO THE REACTION INSTEAD OF MG2+.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC -----
DR EMBL: X69971; CAA49592.1; .
DR HSSP: Q16539; IWRG.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation; Multigene family;
 FT DOMAIN 32 319 PROTEIN KINASE.
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (PROBABLE).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MUTAGEN 61 61 (BY SIMILARITY).
 FT SEQUENCE 372 AA; 42776 MW; 3277355C89F3EBA CMC64;
 SO QUERY MATCH 55.18; Score 1094.5; DB 1; Length 372;
 Best Local Similarity 58.18; Pred. No. 1.7e-64;
 Matches 208; Conservative 63; Mismatches 82; Indels 5; Gaps 4;
 QY 19 VLTGGGVVDFDGFNGNFEITTKYRPPIMPIRGVYGVNLNEMVAVKKIANAF 78
 Db 11 IRTGGRKH--YSMOSLFEIDTKY-VPIKPIGRGATGIVSSVNETEKVAIKKINAF 67
 QY 79 DIYDAKRTLEIKLRHLDHENYIGLRDVIPLPLREFSDVIATLMDTLHQIIRSN 138
 Db 68 ENRIDALRTLEIKLRHLDHENYIGLRDVIPLPLREFSDVIATLMDTLHQIIRSN 127
 QY 139 QGLSEDCQVPTMQLRLKATIHSAANVLRHLSNLLVANCIDIKIDFGIARPN-EN 197
 Db 128 QTLSEDCQVPTMQLRLKATIHSAANVLRHLSNLLVANCIDIKIDFGIARPN-EN 187
 QY 198 ENMEYVYVTRYRRAPELLNSSDYTAIDVMSVGCITFEMLNRRKPLFGKQHVHRIILT 257
 Db 188 QFMETVYVTRYRRAPELLNSSDYTAIDVMSVGCITFEMLNRRKPLFGKQHVHRIILT 247
 QY 258 ELIGTPTPEADIGFLONEDAKRYIRQLPQHPROQLAEVFPVHNPALIDLVMKMLTFDPTRR 317
 Db 248 NILTSQREDEIEFLDNPRARKYIKSLPYSPGTPSRILYPMHAPLAIDLQRLVLDPSKR 307
 QY 318 ITVEALDHPRLAKLHDAGDEIPCPVPSPFDEOQIGEEQIKMIVDEALSNPEYA 375
 Db 308 ISVIEALQHPYMSPLYPDNDPDPAPVPLINDIDED-IGETITREMWMSEILEYHPEEA 364

RESULT 11
 MPK1_ARATH STANDARD; PRT; 370 AA.
 AC Q39021; Q9SY63;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mitogen-activated protein kinase homolog 1 (EC 2.7.1.-) (MAP kinase 1)
 DE (AtMPK1).
 GN MPK1 OR AT1G10210 OR P14N23.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94177172; PubMed=8130795;
 RA Mizoguchi T., Gotoh Y., Nishida E., Yamaguchi-Shinozaki K.,
 RA Hayasaka N., Iwasaki T., Kamada H., Shinozaki K.;
 RT Characterization of two cDNAs that encode MAP kinase homologues in
 RT Arabidopsis thaliana and analysis of the possible role of auxin in
 RT activating such kinase activities in cultured cells.";
 RL Plant J. 5:111-122(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Atafifi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maltl R., Marzilli A.,
 RA Millscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana";
 RL Nature 408:816-820(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RL submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
 CC PHOSPHORYLATION.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE STEM. PRESENT IN THE
 CC LEAF, ROOT AND FLOWER, BUT NOT IN SEEDS.
 CC -1- INDUCTION: BY AUXIN (PROBABLE).
 CC -1- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE. AS WELL AS ON
 CC SERINE RESIDUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -----
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 DR EMBL; D14713; BA03535.1; -;
 DR EMBL; AC005489; AAD32871.1; -;
 DR EMBL; AY059937; AAL24419.1; -;
 DR HSSP; Q16539; IMFC.
 DR InterPro; IPR000572; MAP_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR000719; MAP_kin.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS01351; MAPK; FALSE NEG.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase: Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Multigene family;
 FT DOMAIN 32 319 PROTEIN KINASE.
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MUTAGEN 61 61 (BY SIMILARITY).
 FT SEQUENCE 372 AA; 42776 MW; 3277355C89F3EBA CMC64;
 SO QUERY MATCH 55.18; Score 1094.5; DB 1; Length 372;
 Best Local Similarity 58.18; Pred. No. 1.7e-64;
 Matches 208; Conservative 63; Mismatches 82; Indels 5; Gaps 4;
 QY 19 VLTGGGVVDFDGFNGNFEITTKYRPPIMPIRGVYGVNLNEMVAVKKIANAF 78
 Db 11 IRTGGRKH--YSMOSLFEIDTKY-VPIKPIGRGATGIVSSVNETEKVAIKKINAF 67
 QY 79 DIYDAKRTLEIKLRHLDHENYIGLRDVIPLPLREFSDVIATLMDTLHQIIRSN 138
 Db 68 ENRIDALRTLEIKLRHLDHENYIGLRDVIPLPLREFSDVIATLMDTLHQIIRSN 127
 QY 139 QGLSEDCQVPTMQLRLKATIHSAANVLRHLSNLLVANCIDIKIDFGIARPN-EN 197
 Db 128 QTLSEDCQVPTMQLRLKATIHSAANVLRHLSNLLVANCIDIKIDFGIARPN-EN 187
 QY 198 ENMEYVYVTRYRRAPELLNSSDYTAIDVMSVGCITFEMLNRRKPLFGKQHVHRIILT 257
 Db 188 QFMETVYVTRYRRAPELLNSSDYTAIDVMSVGCITFEMLNRRKPLFGKQHVHRIILT 247
 QY 258 ELIGTPTPEADIGFLONEDAKRYIRQLPQHPROQLAEVFPVHNPALIDLVMKMLTFDPTRR 317
 Db 248 NILTSQREDEIEFLDNPRARKYIKSLPYSPGTPSRILYPMHAPLAIDLQRLVLDPSKR 307
 QY 318 ITVEALDHPRLAKLHDAGDEIPCPVPSPFDEOQIGEEQIKMIVDEALSNPEYA 375
 Db 308 ISVIEALQHPYMSPLYPDNDPDPAPVPLINDIDED-IGETITREMWMSEILEYHPEEA 364

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FT CONFLICT 310 310 V -> A (IN REF. 1).
FT CONFLICT 352 352 M -> I (IN REF. 1).
SQ SEQUENCE 370 AA: 42644 MW: F2962D7881C87A1B CRC64:
Query Match 54.3%; Score 1078; DB 1; Length 370;
Best Local Similarity 57.8%; Pred. No. 2e-63;
Matches 208; Conservative 59; Mismatches 89; Indels 4; Gaps 4;
OY 15 DFPVSLHGGQYQDFGFEFTTTRKPRPIMPICGAGIYCVLTNEMVAVKKI 74
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 6 DPNIGIRNEKH-YFSMWQOLFELDIKYM-PIDIGAGAGVCCSVNSPTNEKVAIKKI 63
OY 75 ANAFDIYMAKRTLRKILRLHLDHENVIGLRDVIPEPLRFESDYIATLMDTDLHQT 134
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 64 HNYENIDILRLRLREIKLRLHRENVIALKDVMPHFKMSFKDYLYELMDTDHQT 123
OY 135 IRSNOGLSEDHCGYFMVQILRLGLKTIHSANVLHRDLKPSNLVANANDLKICDGLARAS 183
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 124 IKSSQVLSNDHCQFLFQLRLGLKTIHSANVLHRDLKPSNLVANANDLKICDGLARAS 183
OY 194 NINENMTEVYVTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQI 253
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 184 NTGQFTEVYVTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQI 253
OY 254 RLTELGLPTFADLGLFQNEKAKRYIRQLPQHPROQLAEVFPVNPDLAIDVDMKLTED 313
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 244 KLIVNIIQSOREDELEFIDNPKAKRYIRSLPYSFGMSLSPGCAHVALAIDLQAKMLYFD 303
OY 314 PTRRITVEALDHPYLAKLNDAGDEPICVPFSPFEOQIGEQIKDMVYQELSLNPE 373
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 304 PSKRISVSEALQHPYMAPLDPNANPPAOVPIIDLVDL-LREEMREMMNEMLHYHPQ 362

RESULT 12
MAPK_PETHY STANDARD: PRT: 384 AA.
AC 040884;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Mitogen-activated protein kinase homolog 1 (EC 2.7.1.1-) (PMEK1).
GN MEK1.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ovule;
RX MEDLINE=95195161; PubMed=7888623;
RA Decrocoq-Ferrant V., Decrocoq S., van Went J., Schmidt E.,
RA Kreis M.;
RT "A homologue of the MAP/ERK family of protein kinase genes is
RT expressed in vegetative and in female reproductive organs of Petunia
RT hybrida."
RL Plant Mol. Biol. 27:339-350(1995).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN VEGETATIVE ORGANS SUCH AS LEAF,
CC ROOT, OR STEM. IN THE REPRODUCTIVE ORGANS, IT IS FOUND IN THE
CC OVARY, BUT NOT IN THE STAMEN.
CC -1- DEVELOPMENTAL STAGE: PRESENT DURING FLOWER DEVELOPMENT PRIOR TO
CC FERTILIZATION. AT EARLY STAGES OF OVULE DEVELOPMENT, THE
CC EXPRESSION IS UNIFORM THROUGHOUT THE OVULE. AT A LATER STAGE, IS
CC LOCALIZED ADJACENT TO THE EMBRYO SAC. WHEN THE FLOWER OPENS AND
CC POLLEN IS RELEASED, IT IS FOUND IN THE WHOLE OVULE AND IN THE
CC OUTER LAYER OF THE PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
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CC -----
DR EMBL: X83440; CAA58466.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; 1.
DR PROSITE: PS01017; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS01018; PROTEIN_KINASE_ST; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 32 319 PROTEIN KINASE.
FT NP_BIND 38 46 ATP (BY SIMILARITY).
FT BINDING 61 61 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 191 191 (BY SIMILARITY).
FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
FT MOD_RES 193 193 (BY SIMILARITY).
SQ SEQUENCE 384 AA: 44444 MW: 7536CG960390EC58 CRC64:
Query Match 54.1%; Score 1075.5; DB 1; Length 384;
Best Local Similarity 57.0%; Pred. No. 3.1e-63;
Matches 204; Conservative 67; Mismatches 82; Indels 5; Gaps 4;
OY 19 VLRHGGQYQDFGFEFTTTRKPRPIMPICGAGIYCVLTNEMVAVKIANAF 78
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 11 IRTPGKHY--YSMWQSLFELDIKTY-VPIKPIGAGAGIYCVSSVNRKENEVAIKKINAF 67
OY 79 DIYMAKRTLRKILRLHLDHENVIGLRDVIPEPLRFESDYIATLMDTDLHQTIRSN 138
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 68 ENRIDALRLRLREIKLRLHRENVIALKDVMPHFKMSFKDYLYELMDTDHQTIRSS 127
OY 139 QGSESDHCQYFMVQILRLGLKTIHSANVLHRDLKPSNLVANANDLKICDGLARPN1-EN 197
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 128 QVLSNDHCQFLFQLRLGLKTIHSANVLHRDLKPSNLVANANDLKICDGLARISGKD 187
OY 198 ENNTEVYVTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQIRLT 257
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 188 QFMTVEYVTRMYRAPPELLNNSDYTAIDVMSVGCIFMELMNRKPLFGKDHVQIRLT 247
OY 258 ELGTPTFADLGLFQNEKAKRYIRQLPQHPROQLAEVFPVNPDLAIDVDMKLTPTTR 317
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 248 NIIGQREDELEFIDNPKAKRYIRSLPYSFGMSLSPGCAHVALAIDLQAKMLYFDSKR 307
OY 318 ILYEALDHPYLAKLNDAGDEPICVPFSPFEOQIGEQIKDMVYQELSLNPEYA 375
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DB 308 ISYMEALQHPYMAPLDPNANPPAOVPIIDLVDL-LVEETIREMMWELIHYHPRA 364

RESULT 13
MPK2_ARATH STANDARD: PRT: 376 AA.
AC 039022; Q9L058;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Mitogen-activated protein kinase homolog 2 (EC 2.7.1.1-) (MAP kinase 2)
DE (AtMPK2).
GN MPK2 OR ATIG59580 OR T30E16.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA MEDLINE=94177172; PubMed=8130795;
 RX Mitozuchi T., Gotoh Y., Nishida E., Yamaguchi-Shinozaki K.,
 RA Hayashida N., Iwasaki T., Kamada H., Shinozaki K.;
 RT "Characterization of two cDNAs that encode MAP kinase homologues in
 RT Arabidopsis thaliana and analysis of the possible role of auxin in
 RT activating such kinase activities in cultured cells.;
 RL Plant J. 5:111-122(1994).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altarfi H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzar L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 RA Miltischer J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 RT SFP consortium (Salk/Stanford/PGSC).";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
 CC PHOSPHORYLATION.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN THE STEM. PRESENT IN THE
 CC LEAF, ROOT AND FLOWER, BUT NOT IN SEEDS.
 CC -1- INDUCTION: BY AUXIN (PROBABLE).
 CC -1- PTM: AUTOPHOSPHORYLATED ON THREONINE AND TYROSINE, AS WELL AS ON
 CC SPRINE RESIDUES.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: D14714; BAA03536.1; -;
 DR EMBL: AC009317; AAF7950.1; -;
 DR EMBL: AT035134; AAK59639.1; -;
 DR HSSP: Q16539; IWFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS01351; MAPK.1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.

KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Phosphorylation; Multigene family.
 FT DOMAIN 32 319 PROTEIN KINASE.
 FT NP_BIND 38 46 ATP (BY SIMILARITY).
 FT BINDING 61 61 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT MOD_RES 191 191 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT MOD_RES 193 193 (BY SIMILARITY).
 FT MOD_RES 193 193 PHOSPHORYLATION (ACTIVATES THE KINASE)
 FT CONFLICT 33 33 (BY SIMILARITY).
 FT CONFLICT 299 299 V -> M (IN REF. 1).
 FT CONFLICT 299 299 M -> I (IN REF. 1).
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 Query Match 53.8%; Score 1069; DB 1; Length 376;
 Best Local Similarity 57.6%; Pred. No. 7.9e-63;
 Matches 209; Conservative 56; Mismatches 94; Indels 4; Gaps 4;
 OY 15 DDPVLTGCGGVVOPDIFGNPFETTKYRPPIMPIGRGAYGVCSVLTMLTENVAVKRI 74
 DB 6 DPNQIRNQGKH-YESMGTLEFIDTKY-VPIKPIGRGAYGVCSVNRSENERVAIKKI 63
 OY 75 ANAFDIYDAKRTLEIRIKLRHLHENVIGLDVIPPRLRRESDVYATATLMDTLHQI 134
 DB 64 HVEFENRIDLATLTLEIKLRHLRHEENVVVKLVANMANKHRSFKDYLVLVETMDTLHQI 123
 OY 135 IRSNGLSDEDCQYRMVOLLGKIKHSANVLRHRLKSNLLVYANCDLKCDEFLAR-P 193
 DB 124 IKSSQVLSNDHCQYFLFOLRLKIKHSANILRHRLKSNLLVYANCDLKCDEFLARTS 183
 OY 194 NIENENKTEYVYTRVYRARELLLNSSDYTAIDVWVSCIPFELMNRKPLFGKDHVQI 253
 DB 184 NTKGFMTEYVYTRVYRARELLLNSSDYTAIDVWVSCIPFELMNRKPLFGKDHVQI 243
 OY 254 RLLELLGTPPEADIGFLQNEDEAKRYIRQLPQPRQQLAEVFPVYVPLAIDLVDKMLTFD 313
 DB 244 KLIIILGSGREEDLEFDINPKAKRYIESLPSPGISRPLPGANVALDILGLMYLVD 303
 OY 314 PTRRTVEALDHPVLAHLHDAGDEPIQVPSFDF-EQGGIGEGQIDMTIYQKLSNP 372
 DB 304 PSKRSTVEALQHPVMAVLPDSANPAVPIDVDEDEDGAEIMELKEMKIHYP 363
 OY 373 EYA 375
 DB 364 EAA 366
 RESULT 14
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 AC Q39027; Q9S114;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mito-gen-activated protein kinase homolog 7 (EC 2.7.1.-) (MAP kinase 7)
 DE (AtMPK7).
 GN MPK7 OR AT2G18170 OR F8D23.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94109583; PubMed=8282107;
 RA Mitozuchi T., Hayashida N., Yamaguchi-Shinozaki K., Kamada H.,
 RA Shinozaki K.;
 RT "ATMPKs: a gene family of plant MAP kinases in Arabidopsis thaliana.";
 RL FEBS Lett. 336:440-444(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;


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RA MEDLINE-20083487. PubMed-10611197.
RX Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Bueli C.R., Ketchum K.A., Lee J.D., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyam L.,
RA Tallon H.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhagen G.P., Preuss D.,
RA Nieman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana."
RL Nature 402:761-768(1999).
CC -1- ENZYME REGULATION: ACTIVATED BY TYROSINE AND THREONINE
CC PHOSPHORYLATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC MAP KINASE SUBFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; D21843; BAA04870.1; -.
CC EMBL; AC007212; AAD31349.1; -.
CC HSSP; Q16539; 1MFC.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR003527; MAP_kin.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; Pkinase; 1.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS01351; MAPK; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Multigene family.
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FT NP_BIND 38 46
FT BINDING 61 61
FT ACT_SITE 158 158
FT MOD_RES 191 191
FT FT
FT MOD_RES 193 193
FT FT
FT CONFLICT 104 104
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FT SEQUENCE 368 AA; 42299 MW; 64587E4CA40C1418 CRC64;
Query Match 53.4%; Score 1061; DB 1; Length 368;
Best Local Similarity 56.7%; Pred. No. 2,6e-62;
Matches 203; Conservative 63; Mismatches 88; Indels 4; Gaps 4;
OY 17 PSYLTGSGYVOEDIFGNEFEITTKYRPPIMPIGAGYGVCSVLTENEMVAVKIAN 76
DB 8 PNGIKOQGRK-H-YYSMWQTLFEIDTRY-VPKIPIGAGYGVCSSTINRETNERVAIKIHN 65
OY 77 AFDIYMDAKRTLRREKILRLHDHENVIGLRVYPLRPFSDVYIANELMDTDLHOIR 136
DB 66 VFNENVADLRRLRLREKILRLHVAHENVIALKDDMLPANNSSFEVDYLVLELMDTDLHOIR 125
OY 137 SNOGLSEPHCOYFMYQLRGKLYISAVNLHRLDSPMLVLANCDLTCDFGLRPMLE 196
DB 126 SSQSLSDBDHCYFLPQLRLGKLYLHSAIMLRDLKPGMLLVANANDKATCDPGLARTISOG 185
OY 197 NEN-MTEYVTRWRAPPELLNNSDYTAIDVWSYGVCTFMELMNRKPLFGKRDHYHQIRL 255

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Db	Accession	Source	Length	Score	DB 1	Length	DB 2	Score	DB 3	DB 4	DB 5	DB 6	DB 7	DB 8	DB 9	DB 10	DB 11	DB 12	DB 13	DB 14	DB 15	DB 16	DB 17	DB 18	DB 19	DB 20	DB 21	DB 22	DB 23	DB 24	DB 25	DB 26	DB 27	DB 28	DB 29	DB 30	DB 31	DB 32	DB 33	DB 34	DB 35	DB 36	DB 37	DB 38	DB 39	DB 40	DB 41	DB 42	DB 43	DB 44	DB 45	DB 46	DB 47	DB 48	DB 49	DB 50	DB 51	DB 52	DB 53	DB 54	DB 55	DB 56	DB 57	DB 58	DB 59	DB 60	DB 61	DB 62	DB 63	DB 64	DB 65	DB 66	DB 67	DB 68	DB 69	DB 70	DB 71	DB 72	DB 73	DB 74	DB 75	DB 76	DB 77	DB 78	DB 79	DB 80	DB 81	DB 82	DB 83	DB 84	DB 85	DB 86	DB 87	DB 88	DB 89	DB 90	DB 91	DB 92	DB 93	DB 94	DB 95	DB 96	DB 97	DB 98	DB 99	DB 100	DB 101	DB 102	DB 103	DB 104	DB 105	DB 106	DB 107	DB 108	DB 109	DB 110	DB 111	DB 112	DB 113	DB 114	DB 115	DB 116	DB 117	DB 118	DB 119	DB 120	DB 121	DB 122	DB 123	DB 124	DB 125	DB 126	DB 127	DB 128	DB 129	DB 130	DB 131	DB 132	DB 133	DB 134	DB 135	DB 136	DB 137	DB 138	DB 139	DB 140	DB 141	DB 142	DB 143	DB 144	DB 145	DB 146	DB 147	DB 148	DB 149	DB 150	DB 151	DB 152	DB 153	DB 154	DB 155	DB 156	DB 157	DB 158	DB 159	DB 160	DB 161	DB 162	DB 163	DB 164	DB 165	DB 166	DB 167	DB 168	DB 169	DB 170	DB 171	DB 172	DB 173	DB 174	DB 175	DB 176	DB 177	DB 178	DB 179	DB 180	DB 181	DB 182	DB 183	DB 184	DB 185	DB 186	DB 187	DB 188	DB 189	DB 190	DB 191	DB 192	DB 193	DB 194	DB 195	DB 196	DB 197	DB 198	DB 199	DB 200	DB 201	DB 202	DB 203	DB 204	DB 205	DB 206	DB 207	DB 208	DB 209	DB 210	DB 211	DB 212	DB 213	DB 214	DB 215	DB 216	DB 217	DB 218	DB 219	DB 220	DB 221	DB 222	DB 223	DB 224	DB 225	DB 226	DB 227	DB 228	DB 229	DB 230	DB 231	DB 232	DB 233	DB 234	DB 235	DB 236	DB 237	DB 238	DB 239	DB 240	DB 241	DB 242	DB 243	DB 244	DB 245	DB 246	DB 247	DB 248	DB 249	DB 250	DB 251	DB 252	DB 253	DB 254	DB 255	DB 256	DB 257	DB 258	DB 259	DB 260	DB 261	DB 262	DB 263	DB 264	DB 265	DB 266	DB 267	DB 268	DB 269	DB 270	DB 271	DB 272	DB 273	DB 274	DB 275	DB 276	DB 277	DB 278	DB 279	DB 280	DB 281	DB 282	DB 283	DB 284	DB 285	DB 286	DB 287	DB 288	DB 289	DB 290	DB 291	DB 292	DB 293	DB 294	DB 295	DB 296	DB 297	DB 298	DB 299	DB 300	DB 301	DB 302	DB 303	DB 304	DB 305	DB 306	DB 307	DB 308	DB 309	DB 310	DB 311	DB 312	DB 313	DB 314	DB 315	DB 316	DB 317	DB 318	DB 319	DB 320	DB 321	DB 322	DB 323	DB 324	DB 325	DB 326	DB 327	DB 328	DB 329	DB 330	DB 331	DB 332	DB 333	DB 334	DB 335	DB 336	DB 337	DB 338	DB 339	DB 340	DB 341	DB 342	DB 343	DB 344	DB 345	DB 346	DB 347	DB 348	DB 349	DB 350	DB 351	DB 352	DB 353	DB 354	DB 355	DB 356	DB 357	DB 358	DB 359	DB 360	DB 361	DB 362	DB 363	DB 364	DB 365	DB 366	DB 367	DB 368	DB 369	DB 370	DB 371	DB 372	DB 373	DB 374	DB 375	DB 376	DB 377	DB 378	DB 379	DB 380	DB 381	DB 382	DB 383	DB 384	DB 385	DB 386	DB 387	DB 388	DB 389	DB 390	DB 391	DB 392	DB 393	DB 394	DB 395	DB 396	DB 397	DB 398	DB 399	DB 400	DB 401	DB 402	DB 403	DB 404	DB 405	DB 406	DB 407	DB 408	DB 409	DB 410	DB 411	DB 412	DB 413	DB 414	DB 415
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[illegible]

Search completed: May 20, 2003, 00:22:20
Job time : 39 secs

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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:00:32 : Search time 60 Seconds
(without alignments)
1287.794 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
Sequence: 1 MADANMAGGQGFDPSPVL.....EQIKDMYQPALSLNPEYA 375

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp Unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	10	040598
2	1958	98.5	375	10	08W406
3	1861	93.7	375	10	09LK22
4	1650	83.0	371	10	004694
5	1641	82.6	371	10	09M6S1
6	1635	82.3	365	10	09XGV8
7	1634	82.2	371	10	024077
8	1490	75.0	369	10	09AXF2
9	1487	74.8	369	10	09FQM3
10	1483.5	74.7	394	10	004LK21
11	1482	74.6	393	10	004362
12	1473	74.1	369	10	043379
13	1472.5	74.1	399	10	09ZM75
14	1472	74.1	369	10	09FSE6
15	1471.5	74.1	389	10	09M534
16	1468	73.9	369	10	081599

17	1445	72.7	406	10	09ZM76	09ZM76 zea mays (m
18	1301	65.5	371	10	09AYN8	09AYN8 nicotiana t
19	1286	64.7	374	10	09ZP91	09ZP91 medicago sa
20	1285	64.7	363	10	09LK09	09LK09 arabidopsis
21	1279.5	64.4	393	10	09M175	09M175 arabidopsis
22	1258.5	63.3	369	10	09LMM5	09LMM5 arabidopsis
23	1232.5	62.0	389	10	09FX77	09FX77 chlamydomon
24	1219	61.3	406	10	08Z361	08Z361 arabidopsis
25	1112	56.0	370	10	09M545	09M545 oryza sativ
26	1087	54.7	372	10	09M6R8	09M6R8 pisum sativ
27	1085	54.6	369	10	09FQM2	09FQM2 oryza sativ
28	1076	54.2	369	10	09SMA9	09SMA9 oryza sativ
29	1034.5	52.1	368	10	09XFP95	09XFP95 prunus ame
30	1002	50.4	361	10	023236	023236 arabidopsis
31	957	48.2	265	10	08S376	08S376 oryza sativ
32	931	46.9	354	3	09Q0Y5	09Q0Y5 ustilago ma
33	927	46.7	351	3	042781	042781 pneumocysti
34	924	46.5	356	3	092246	092246 magnaporthe
35	921	46.4	352	3	09C1E0	09C1E0 neurospora
36	921	46.4	355	3	09C1I9	09C1I9 blumeria gr
37	920	46.3	355	3	09HG02	09HG02 fusarium ox
38	918	46.2	355	3	09C4B0	09C4B0 colletotric
39	918	46.2	355	3	09W0V9	09W0V9 glomerella
40	916	46.1	355	3	000859	000859 fusarium so
41	914	46.0	352	3	096X31	096X31 pyrenophora
42	914	46.0	355	3	09HG08	09HG08 botrytis ci
43	914	46.0	355	3	08X1A2	08X1A2 gibberella
44	907	45.6	355	3	09C137	09C137 gibberella
45	906	45.6	352	3	09UVN7	09UVN7 cochliobolus

ALIGNMENTS

RESULT 1
ID Q40598 PRELIMINARY; PRT; 375 AA.
AC Q40598;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE WIPK.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxId=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96123271; PubMed=8533090;
RA Seo S., Okamoto M., Sato H., Ishizuka K., Sano H., Ohashi Y.,
RT "Tobacco MAP kinase: a possible mediator in wound signal transduction
RT pathways.";
RL Science 270:1988-1992(1995).
CC -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D61377; BAA09600.1; -;
DR HSP: Q16539; IWP.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Euk_Pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SO SEQUENCE 375 AA; 42853 MW; 23480DEBA1EACBD8 CRC64;
Query Match 100.0%; Score 1987; DB 10; Length 375;
Best Local Similarity 100.0%; Pred. No. 9,8e-162;
Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60
 QY 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 QY 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRDLKPSMLLVAN 180
 DB 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRDLKPSMLLVAN 180
 QY 181 CDLKICDGLARPIENENMTYVTRMYRAPPELLNSSDYTAIDVWSVCIFMELMNR 240
 DB 181 CDLKICDGLARPIENENMTYVTRMYRAPPELLNSSDYTAIDVWSVCIFMELMNR 240
 QY 241 KPLFGGDHWHQIRLTELSTPTADLGLQNEADAKRYIRQLPQHPQOLAEEVPPHNP 300
 DB 241 KPLFGGDHWHQIRLTELSTPTADLGLQNEADAKRYIRQLPQHPQOLAEEVPPHNP 300
 QY 301 LAIDLVDKMLTFDPTRRITVEALDHPYLAHLADGDEPICPVPSFDEQOIGEEQIK 360
 DB 301 LAIDLVDKMLTFDPTRRITVEALDHPYLAHLADGDEPICPVPSFDEQOIGEEQIK 360
 QY 361 DMITYQEALSLNPEYA 375
 DB 361 DMITYQEALSLNPEYA 375

RESULT 2

ID 08W406 PRELIMINARY; PRT; 375 AA.
 AC 08W406;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Wound induced protein kinase.
 GN WIPK.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sano H., Yap Y.K.;
 RT "Genome organisation of WIPK gene in tobacco."
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB052964; BAB79636.1; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR SMART: SM00219; TYKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW kinase.
 SQ SEQUENCE 375 AA; 42898 MW; 9BA49C8C39E1C88F CRC64;

Query Match 98.5%; Score 1958; DB 10; Length 375;
 Best Local Similarity 98.4%; Pred. No. 3e-159;
 Matches 369; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60

QY 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 QY 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRDLKPSMLLVAN 180
 DB 121 YIATELMDTDLHQIIRSNQGLSEDCQYFMQYLLRGLKYHSANVLRDLKPSMLLVAN 180
 QY 181 CDLKICDGLARPIENENMTYVTRMYRAPPELLNSSDYTAIDVWSVCIFMELMNR 240
 DB 181 CDLKICDGLARPIENENMTYVTRMYRAPPELLNSSDYTAIDVWSVCIFMELMNR 240
 QY 241 KPLFGGDHWHQIRLTELSTPTADLGLQNEADAKRYIRQLPQHPQOLAEEVPPHNP 300
 DB 241 KPLFGGDHWHQIRLTELSTPTADLGLQNEADAKRYIRQLPQHPQOLAEEVPPHNP 300
 QY 301 LAIDLVDKMLTFDPTRRITVEALDHPYLAHLADGDEPICPVPSFDEQOIGEEQIK 360
 DB 301 LAIDLVDKMLTFDPTRRITVEALDHPYLAHLADGDEPICPVPSFDEQOIGEEQIK 360
 QY 361 DMITYQEALSLNPEYA 375
 DB 361 DMITYQEALSLNPEYA 375

RESULT 3

ID 09LKZ2 PRELIMINARY; PRT; 375 AA.
 AC 09LKZ2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE MAP kinase 1.
 GN MK1.
 OS Capsicum annuum (bell pepper).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
 OX NCBI_TaxID=4072;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Back K., Han O., Shin H.-J., Kim K.-U;
 RT "Molecular cloning and cultivar specific expression of MAP kinase from Capsicum annuum."
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF247135; AAF81419.1; -
 DR HSSP: Q16539; IWFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 375 AA; 42954 MW; AE78396ZACS240C4 CRC64;

Query Match 93.7%; Score 1861; DB 10; Length 375;
 Best Local Similarity 92.5%; Pred. No. 5.8e-151;
 Matches 347; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60
 DB 1 MADANMGAGGQFPDPFSVLTHGGQYVQDFDIFGNFEITTKYRPPIMPGRGAGYICSV 60
 QY 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120
 DB 61 LNTLELNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVIGLRVYIPPLRERSDV 120

Qy	121	YIATIELMDTDLHOIIRSNOCUSLSEBHCQYFMYOLLRIKLTHTSHANVLHRDLKPSNLLYMAN	180
	121	YIATIELMDTDLHOIIRSNOCUSLSEBHCQYFMYOLLRIKLTHTSHANVLHRDLKPSNLLYMAN	180
Db	121	YIATIELMDTDLHOIIRSNOCUSLSEBHCQYFMYOLLRIKLTHTSHANVIRHDLKPSNLLYMAN	180
Qy	181	CDKICDCEGLARPNIEENMNT EYVTRMYRAPPELLNSSDYTAIDVWSGCI.FEMELMNR	240
	181	CDKICDCEGLARPNIEENMNT EYVTRMYRAPPELLNSSDYTAIDVWSGCI.FEMELMNR	240
Db	181	CDKICDCEGLARPNIEENMNT EYVTRMYRAPPELLNSSDYTAIDVWSGCI.FEMELMNR	240
Qy	241	KPLFGKDWHQIRLLTTELLGTPTEADLGLONEDAKRYIROL.POHPRQOLAEPFPHVP	300
	241	KPLFGKDWHQIRLLTTELLGTPTEADLGLONEDAKRYIROL.POHPRQOLAEPFPHVP	300
Db	241	KPLFGKDWHQIRLLTTELLGTPTEADLGLONEDAKRYIROL.POHPRQOLAEPFPHVP	300
Qy	301	LAIIDVVKMLTFDPTRRTIYVEALADHYLAKLDAGCEPITCAPSPESDFPQOIGIGEBOIK	360
	301	LAIIDVVKMLTFDPTRRTIYVEALADHYLAKLDAGCEPITCAPSPESDFPQOIGIGEBOIK	360
Db	301	LAIIDVVKMLTLNPTGATITVEALAHPTYLAKLDADADEPVPFSPESDFPQOIGIGEBOIK	360
Qy	361	DMIVQEALSLNPEYA 375	
	361	DMIVQEALSLNPEYA 375	
Db	361	DMIVQEALSLNPEYA 375	

RESULT 4	ID	004694	PRELIMINARY;	PRT:	371 AA.
AC	004694;				
DT	01-JUL-1997	(TREMBLrel. 04, Created)			
DT	01-JUL-1997	(TREMBLrel. 04, Last sequence update)			
DT	01-MAR-2002	(TREMBLrel. 20, Last annotation update)			
DE	MAP kinase I.				
OS	Petroselinum crispum (Parsley) (Petroselinum hortense).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.				
OX	NCBI_Taxid=4043;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-97342856; PubMed-9197271;				
RA	Ligterink W., Kroj T., zur Nieden U., Hirt H., Scheel D.;				
RT	"Receptor-mediated activation of a MAP kinase in pathogen defense of				
RT	plants."				
SC	Science 276:2054-2057(1997).				
RL	-I SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.				
DR	HMSL; Y12785; CAAT3323.1; "				
DR	HSSP; O16539; IMWC.				
DR	Interpro: IPR000719; Euk_kinase.				
DR	Interpro: IPR003527; MAP_kin.				
DR	Interpro: IPR002290; Ser_Chr_kinase.				
DR	Pfam: PF00069; kinase.1.				
DR	ProDom: PD000001; Euk_kinase.1.				
DR	SMART: SM00220; S_TKc.1.				
DR	PROSITE: PS01351; MAPK; UNKNOWN.1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.				
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM.1.				
DR	PROSITE: PS00108; PROTEIN_KINASE_ST.1.				
DR	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.				
QO	SEQUENCE 371 AA; 42794 MW; 6BDA68328221B3E8 CnC64;				

Query Match	83.0%;	Score 1650;	DB 10;	Length 371;
Best Local Similarity	81.7%;	Pred. No. 6.4e-133;		
Matches 300;	Conservative 39;	Mismatches 28;	Indels 0;	Gaps 0;

QY	9	GGGQPPDEPSVLTGGGVVOVEDIFENFEITTKYPPIMPIGRGAGVYVCVSLNLELNM	68
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	5	GDGQYTERPALOTHOHGOYIYINIEGNLOYVKKYPPIMPIGRGAGVYVCVSLNLELNM	64
QY	69	VAVKKIANAFDIYMAKTKTLREIKLRLHLDHENVIGLROVYPPULREESDYIATELMD	128
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	65	VAVKKIANAFNYMDAKTKTLREIKLRLHLDHENVIAITDYVPPULREETDYIATELMD	124
QY	129	TDLHQIINSNOGLSEDHCOQYFMYQLRLRIKLYHSANVYLRDLKPSNLLVNAWCDKICDF	188
		: : : : : : : : : : : : : : : : : : : : : : : : :	
Db	125	TDLHQIINSNOGLSEHCOQYFYLRLRLKLYHSANIIYLRDLKPSNLLVNAWCDKICDF	184

QY	189	GLAPRINENEMEEYVUTRYM	RAPELLNSDYTA	LAIDVMSVGC	IFMELNNKRP	LFEGKD	248
	185	: : :					
Db	185	GLAHNNDEEMEEYVUTRYM <td>RAPELLNSDYTA<th>LAIDVMSVGC</th><th>IYMELNNKRP</th><th>LFEGKD</th><th>244</th></td>	RAPELLNSDYTA <th>LAIDVMSVGC</th> <th>IYMELNNKRP</th> <th>LFEGKD</th> <th>244</th>	LAIDVMSVGC	IYMELNNKRP	LFEGKD	244
QY	249	HVHDIRLLTELLGPRTEADIGF	LIONEDAKRYTOLPHR	PROOLAEPYRHNPLA	IDLVDR		308
	245	: : :					
Db	245	HVHOMRLLTELLGSTRTEADIGF	VANNEDEAKRYTOLPHR	PROOLRYOLPHVNRPLA	IDLVDR		304
QY	309	MLTDPFRIRITVEALDHNRYLAK	LINDGADDEPRISVPRSP	DFEEOGIGLEOIK	IMITYOVAL		368
	305	: : :					
Db	305	MLTFDPKSRITVEALDHNRYLAK	RINDIADDEPRISKTPRS	FEFFETLANHGEQIK	IMITYOVAL		364
QY	369	SLNDEYA	375				
	365						
Db	365	AFNPDCA	371				

RESULT	5
09M6S1	PRELIMINARY; PRT; 371 AA.
ID	09M6S1
AC	09M6S1;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	MAP kinase 3.
GN	MAPK3.
OS	Pisum sativum (Garden pea).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Eumariophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX	NCBI_TaxID=3888;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SRRIN-CV_ALASKA; TISSUE=OVARY;
RX	MEDLINE=21003323; PubMed=11117261;
RA	Marcoete M.J., Carbonell J.
RT	"Transient expression of a pea MAP kinase gene induced by gibberellin acid and 6-benzyladenine in unimplanted pea ovaries."
RL	Plant Mol. Biol. 44:177-186(2000).
CC	1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR	EMBL; AF153061; AAF73236.1; ..
DR	HSSP; Q16539; IWFC.
DR	InterPro; IPR000719; Euk_pkinase.
DR	InterPro; IPR003527; MAP_kin.
DR	InterPro; IPR002290; Ser_thr_pkinase.
DR	Pfam; PF00069; pkinase.1;
DR	ProDom; PD000001; Euk_pkinase.1.
DR	SMART; SM00220; S_TKC.1.
DR	PROSITE; PS01351; MAPK; UNKNOWN.1.
DR	PROSITE; PS00107; PROTEIN_KINASE_ADP.1.
DR	PROSITE; PSS0011; PROTEIN_KINASE_DOM.1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST.1.
QO	ATP-binding; Kinase; Serine/threonine protein kinase; Transferase.
QO	SEQUENCE 371 AA; 42919 MW; A6FA22D295CF468C CRC4;

Query Match	82.6%;	Score 1641;	DB 10;	Length 371;
Best Local Similarity	83.1%;	Pred. No. 3.8e-132;		
Matches 300: Conservative	37;	Mismatches 24;	Indels 0;	Gaps 0;

Db 191 MENDEMEYVTRMYRAPELLNNSDYTSADVWSVGCIFMELNKKRPLFGKDHVQMR 250
 QY 255 LTTELLGPTPEADGFLONEDAKRYIROLPOHPRQOLAEPVPHVPLAIDLVDKMLTFDP 314
 Db 251 LTTELLGPTPEADGFLONEDAKRYIROLPOHPRQOLAEPVPHVPLAIDLVDKMLTFDP 310
 QY 315 TRRTIVEBALDHPYLAUKLHDAGDEPICVPSPFDEOQIGEEQIKDMITOEALSLNDEY 374
 Db 311 TRRTIVEBALDHPYLAUKLHDAGDEPICVPSPFDEOQIGEEQIKDMITOEALSLNDEY 370
 QY 375 A 375
 Db 371 A 371

RESULT 6
 Q9XG78 PRELIMINARY: PRT: 365 AA.
 ID Q9XG78
 AC Q9XG78
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE MAP kinase.
 OS Ipomoea batatas (Sweet potato) (Batale).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Asteridae; eusterids I; Solanales; Convolvulaceae; Ipomoea.
 NCBI_TaxID=4120;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, TAINONG 57; TISSUE=LEAF;
 RA To K.Y., Suen D.F., Chen S.C.G.;
 RT "Cloning Of A Sweet Potato Leaf cDNA (Accession No. AF149424) Encoding
 RT Mitogen-Activated Protein Kinase. (PGR99-135).";
 RL Plant Physiol. 121:312-312(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF149424; AAD37790.1; -
 DR HSSP: P27703; IERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 365 AA; 41745 MW; 4A2998BA81178427 CRC64;
 SQ
 Query Match 82.3%; Score 1635; DB 10; Length 365;
 Best Local Similarity 82.8%; Pred. No. 1.2e-131;
 Matches 304; Conservative 35; Mismatches 24; Indels 4; Gaps 2;

Db 240 HVHQRLLTELLGPTPEADGFLONEDAKRYIROLPOHPRQOLAEPVPHVPLAIDLVDK 299
 QY 309 MLTFDPTRTRIVEBALDHPYLAUKLHDAGDEPICVPSPFDEOQIGEEQIKDMITOEAL 368
 Db 300 MLTFDPTRTRIVEBALDHPYLAUKLHDAGDEPICVPSPFDEOQIGEEQIKDMITOEAL 358
 QY 369 SLNDEYA 375
 Db 359 AMNPGYA 365

RESULT 7
 Q24077 PRELIMINARY: PRT: 371 AA.
 ID Q24077
 AC Q24077
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Protein kinase.
 GN MMR4.
 OS Medicago sativa (Alfalfa).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eusterids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae; Medicago.
 NCBI_TaxID=3879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=97008170; PubMed=8855346;
 RA Jonak C., Kiegl S., Ligerling W., Barker P., Huskisson N., Hirt H.;
 RT "signaling in plants: a mitogen-activated protein kinase pathway is
 RT activated by cold and drought.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:11274-11279(1996).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X82270; CA57721.1; -
 DR HSSP: Q16539; IMFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR ProDom: PD000001; Euk_pkinase.1.
 DR SMART: SM00220; S_TKc.1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00101; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 371 AA; 42963 MW; 8CCC390454E4350E CRC64;
 SQ
 Query Match 82.2%; Score 1634; DB 10; Length 371;
 Best Local Similarity 82.8%; Pred. No. 1.5e-131;
 Matches 299; Conservative 38; Mismatches 24; Indels 0; Gaps 0;

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Db      311  TRRTVEALAHPLYLEKLDHVADEP ICMEPISFEEOQHIDDEQ IKEMITYREALALNPEY 370
Oy      375  A 375
Db      371  A 371

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RESULT 8
Q9AXF2
ID Q9AXF2 PRELIMINARY; PRT; 369 AA.

DR 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MAP_Kinase BIK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. YUANFENGZAO;
RA Song F., Goodman R.M.;
RT "OSBIK1, a novel MAP kinase from rice that is involved in systemic
RT acquired resistance";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC EMBL: AF32873; AAK01710.1; -.
DR HSSP: Q16539; IMFC.
DR InterPro: IPR000719; MAP_kinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYRCK; 1.
DR PROSITE: PS01351; MARK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
QW SEQUENCE 369 AA: 43023 MW: 417D88EB32635F2D3 CAC64.

Query Match	75.0%	Score 1490;	DB 10;	Length 369;
Best Local Similarity	72.3%	Pred. No. 3.1e-119;		
Matches 264;	Conservative 59;	Mismatches 42;	Indels 0;	Gaps 0;

QY	10	GGGPPDPSPYLTGGGYVQVEDIFENFEPIITTKYPPMPIMGKAGYGVGVLTUETLWEM	69
Db	3	GAPAAEPRPMTTGGGRYLLVDIFGNKREVIYNKKQPPIMPIGRAGYGVGVSMNFEETEM	62
QY	70	AVKIIAFAFDYMDAKKTAEIKILRLHLDHENYIGLRDVIYPPRLREFSDVIYATLMDT	129
Db	63	AIKKIIAFAFNMDAKKTLEIEKILRLHLDHENYIGIDVIYPPPIQAFNFDVIYATLMDT	122
QY	130	DLHIIIRSNQGLSEDCQYEMFYQLRLCKYIHSANVYLRDLKPSNLVYANCDLKCIDFG	189
Db	123	DLHHIIRSNQGLSEHCQYFLYQLRLCKYIHSANVYLRDLKPSNLVYANCDLKCIDFG	182
QY	190	LARININENMTEVYVTRKTPRAPRLILNSSDYPAIDVMSVGCIFMELANRKPFLGGKH	249
Db	183	LARSSSDMDMTEVYVTRKTPRAPRLILNSTDYSAIDVMSVGCIFMELINRQPLFGGRH	242
QY	250	VHQIRLLTELSTPTTEADLFLQIOMEDAKRYTRLOLPPQHRPOOLAEVFPYHNPVLAIDLVDK	309
Db	243	MHQIRLLTEVYIGPTDDELGIIRINEDAKKIMRHNPQYPRRTFISMFPYRQPALDLIERM	302
QY	310	LTPPRTKRIRIYEALDHPRYLAKLHADGDEPTCPVPSSDFEQQIGEEQIKDMMYQEALS	369
Db	303	LTPPRLQRIIYEALDHPRYLRLHLDIADECIPEPSSDFEQQALNDDKQKLTIFNAIE	362

QY	370	LNPEY	374
		: :	
Db	363	MNPNE	367

RESULT 9
Q9FQM3
ID Q9FQM3 PRELIMINARY; PRT; 369 AA

DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE MAP_Kinase_1 (MAP_Kinase MAPK3a).
GN MAPK5.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; *Oryza*.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RP Wen J.-O., Imai R.;
RA "A MAP kinase cascade component, OSMAP1 was induced by chilling stress
RT in rice.";
RL In rice.";
RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RP Xiong L., Qi M., Yang Y.;
RA "Molecular cloning and characterization of a novel MAP kinase,
RT OSMAPK5, in rice.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF216315; AAC40579.1; -
DR EMBL: AF479883; AAL87689.1; -
DR HSSP: Q16539; 1WFC.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: pD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR SMART: SM00219; TYKc; 1.
DR PROSITE: PS001351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Transferase.
KW SEQUENCE 369 AA; 4295 MW; 417D81732635F2D3 CRC64;

Query Match	74.8%	Score 1487	DB 10	Length 369
Best Local Similarly	72.7%	Pred. No. 5.6e119		
Matches 264	Conservative 58	Mismatches 41	Indels 0	Gaps 0

[illegible]

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QY 310 LTFDPRTIYVEALDHPYLAKLHDAGDEPICVPFSPFDEQOIGEOIKDMIOEALS 369
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 303 LTFNPLRIYVEALDHPYLAKLHDAGDEPICLEPFSEFQKALNEDOMKOLINNEAIE 362
QY 370 LNP 372
      |||
Db 363 MNP 365

RESULT 10
09LKZ1 PRELIMINARY: PRT: 394 AA.
ID 09LKZ1
AC 09LKZ1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE MAP kinase 2.
GN MK2.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RA Back K., Han O., Shin H.-J., Kim K.-U.;
RT "Molecular cloning and cultivar specific expression of MAP kinase from
RT Capsicum annuum."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF247136; AAF81420.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 394 AA; 45196 MW; 788FF8C76D383C15 CRC64;

Query Match 74.7%; Score 1483.5; DB 10; Length 394;
Best Local Similarity 75.0%; Pred. No. 1.2e-118;
Matches 270; Conservative 43; Mismatches 46; Indels 1; Gaps 1;

QY 15 DEPSVLTGGGVQEDTGNFEFTTKRPPIMPIGRAGYIGSVLTTELNEMVAVAKI 74
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 NIPATLSGGRFQYINFGNVEYAKYKPPIMPIGRAGYIGSVLTSELNEHVATKI 92
QY 75 ANADIVYADARTLREIKLRLHDHENYIGLDVYPPRLREESVYVYATLMDTDLQI 134
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 93 ANADINKIDAKRTLEIKLRLHDHENYVAILRDIIPORAFANDVYIAYELMDTDLQI 152
QY 135 IRSNOGLSEHCQYFMQQLGLKYLHGSANYLHRLDKPSNLLVYANCDLKCDFGLAPN 194
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 153 IRSNOGLSEHCQYFELQYILRLKYLHGSANYLHRLDKPSNLLVYANCDLKCDFGLAVT 212
QY 195 IENENMTEYVYTRWYRAPELLNSSDYTAALDVMSVGCIFEMELNKRKLFGSKDHVHQR 254
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 213 SETPFMEYVYTRWYRAPELLNSSDYTAALDVMSVGCIFEMELNKRKLFGSKDHVHQR 272
QY 255 LTELGLPTFADIGFLONEDAKRYIRLPORHQALEVPVPHVPLAIDLVDKMLTFDP 314
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 273 LLMELIGPSSAEKMEFL-NEAKRYIRQLPLYRROSEYKRPVHPAIDLVKMLTFDP 331
QY 315 TRITVEALDHPYLAKLHDAGDEPICVPFSPFDEQOIGEOIKDMIOEALSINPEY 374
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 332 RRRLVEALDHPYLAKLHDAGDEPICVPFSPFDEQOIGEOIKDMIOEALSINPEY 391
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RESULT 11
004362 PRELIMINARY: PRT: 393 AA.
ID 004362
AC 004362;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Salicylic acid-activated MAP kinase.
GN NTSIPK.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=XANTHI NC.
RA Zhang S., Kleesig D.F.;
RT "Salicylic acid activates a 48-kilodalton MAP kinase in tobacco."
RL Plant Cell 9:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U94192; AAB58396.1; -.
DR HSSP: P27703; IERK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003527; MAP_kin.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS01351; MAPK; UNKNOWN_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 393 AA; 45162 MW; 4C707023F1E0904C CRC64;

Query Match 74.6%; Score 1482; DB 10; Length 393;
Best Local Similarity 71.5%; Pred. No. 1.6e-118;
Matches 274; Conservative 46; Mismatches 51; Indels 12; Gaps 2;

QY 3 DANKAGGGGPP-----DEPSVLTGGGVQEDTGNFEFTTKRPPIMPIGR 51
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 DTMSDAGAEPPPARPOQVAGMDNIPATLSHGRTQYINFGNVEYAKYKPPILPIGK 68
QY 52 GAYGIVSVLTTELNEMVAVAKIANAFDIYDAKRTLEIKLRLHDHENYIGLDVYIP 111
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 GAYGIVCALNSETEIENVAIKKIANAFDNKIDAKRTLEIKLRLHDHENYVAILRDIIP 128
QY 112 PLRREFSVYVYATLMDTDLQIIRSNOGLSEHCQYFMQQLGLKYLHGSANYLHRLDK 171
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 POREAFNDVYVYIAYELMDTDLQIIRSNOGLSEHCQYFELQYILRLKYLHGSANYLHRLDK 188
QY 172 PSNLLVYANCDLKCDFGLAPNTENEMTEYVYTRWYRAPELLNSSDYTAALDVMSV 231
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 189 PSNLLVYANCDLKCDFGLAPNTSETDPFMEYVYTRWYRAPELLNSSDYTAALDVMSV 248
QY 232 CIFMELNKRKLFGSKDHVHQRILTELGLPTFADIGFLONEDAKRYIRLPORHQA 291
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 249 CIFMELMDRKPLFGSDHGHQRLIMELIGPSSAEKMEFL-NEAKRYIRQLPLYRROSE 307
QY 292 AEVPPVPHVPLAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPFSPFDEQ 351
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 308 TEKPPVHPVPTAIDLVKMLTFDPDRRITVEGALAHPLYLNSLHDSIDPCMTPEFDEQ 367
QY 352 OGIGEOIKDMIOEALSINPEY 374
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 368 HALTEQMKELIYRESLAFNPEY 390

RESULT 12
043379 PRELIMINARY: PRT: 369 AA.
ID 043379
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AC Q43379;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, last sequence update)
 DE 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 GN MAP kinase.
 OS Avena sativa (Oat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Avenae; Avena.
 OX NCBI_TaxID=4498;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, RHANON; TISSUE=ALEURONE;
 RX MEDLINE=95284341; PubMed=7766874;
 RA Huttly A.K., Phillips A.L.;
 RT "glibetellin regulated expression in oat aleurone cells of two kinases
 RT that hsov homology to nap kinase and a ribosomal protein kinase.";
 RL Plant Mol. Biol. 27:1043-1052(1995).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: X79993; CAA56314.1; -.
 DR HSSP: Q16539; IMFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding: Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 369 AA; 42871 MW; 2A76A350A867A63f CRC64.

Query Match 74.1%; Score 1473; DB 10; Length 369;
 Best Local Similarity 72.9%; Pred. No. 8.8e-118;
 Matches 266; Conservative 52; Mismatches 47; Indels 0; Gaps 0;

QY 10 GGQFPDFPSVLTHGGQYVOFDIFGNFFETTKYRPPIMPIGAGAYGYCVLTELNEKV 69
 DB 3 GAPVAEFPPTMGGRFLLYNIFGNQFETSKYQPPIMFIGAGAYGYCVANFETREKV 62
 QY 70 AVKRIANAFDIYMDAKRTLRREIKLRHLDHENYIGLRDVIYPPILRRFSQVYIATELMDT 129
 DB 63 AIKRIANAFDNMDAKRTLRREIKLRHLDHENYIGLRDVIYPPISIQSEFNDYIATELMDT 122
 QY 130 DLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANVLRHDLKPSNLLVANCCLKICDFG 189
 DB 123 DLHNIIRSNQGLSEDCQYFMYQLLRGLKYIHSANVLRHDLKPSNLLVANCCLKICDFG 182
 QY 190 LARPPIENMTTEYVYTWYRAPPELLNSSDYTAIDVWVSGCIPMELNKRPLFGGKDH 249
 DB 183 LARPSSEDDMTTEYVYTWYRAPPELLNSTDVSAIDVWVSGCIPMELNKRPLFGGRDH 242
 QY 250 VHOIRLTELGTPTADLGLFQNEEDAKRYIRQLPQHRQOLAEEFPHVNPALIDLVKM 309
 DB 243 MHQMLLIEVIGTPTDDDLGFRINEDARRYMHLRQFRRRRPGQFRKVPQAPALDIEM 302
 QY 310 LTFDPTRITVEALRDHYLLAKHDAGDEPICVPVPSDFEEOGIGEOIKIMYOEALIS 369
 DB 303 LTFNDRITVEALEHLYERLHDVADPCTDPSDFEQHPLTEMDQMKOLINEALE 362
 QY 370 LNPEY 374
 DB 363 LNPNF 367

RESULT 13
 Q9ZMJ5 PRELIMINARY; PRT; 399 AA.
 AC Q9ZMJ5;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 DE MAP kinase 5.
 GN ZMMPK5.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoidae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HONEYBUNTAM;
 RX MEDLINE=20055759; PubMed=10589842;
 RA Berberich T., Sano H., Kusano T.;
 RT "Involvement of a MAP kinase, ZMMPK5, in senescence and recovery from
 RT low-temperature stress in maize.";
 RL Mol. Gen. Genet. 262:534-542(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB016802; BAA74734.1; -.
 DR HSSP: P27703; 1ERK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding: Kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 399 AA; 44891 MW; 04982715587106C9 CRC64.

Query Match 74.1%; Score 1472.5; DB 10; Length 399;
 Best Local Similarity 71.2%; Pred. No. 1.1e-117;
 Matches 277; Conservative 45; Mismatches 50; Indels 17; Gaps 4;

QY 1 MADANMAGCGGQFPDP-----SVLTHGGQYVOFDIFGNFFETTKYRPPI 46
 DB 12 MEAGAGG-GGGQPPQOPLRPVGGGYLMDNIQATLSHGGRFIOYNIFGNVFEYTAKKPPL 70
 QY 47 MDIGGAGYGYCVSINTE-LNEMVAVKRIANAFDIYMDAKRTLRREIKLRHLDHENYIGL 105
 DB 71 LPIGGAGYGYCVSAVSEFAAEGGSKRIANAFDNKIDAKRTLRREIKLRHMDHENYIAI 130
 QY 106 RQVYPPILRRFSQVYIATELMDTLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANV 165
 DB 131 RQIIPPQQAAPNDVYIATELMDTLHQIIRSNQGLSEDCQYFMYQLLRGLKYIHSANV 190
 QY 166 LHRDLKPSNLLVANCCLKICDFGLARPIENENMTTEYVYTWYRAPPELLNSSDYTAI 225
 DB 191 LHRDLKPSNLLVANCCLKICDFGLARTTSSEDFMTTEYVYTWYRAPPELLNSSDYTAI 250
 QY 226 DVWVSGCIPMELNKRPLFGGKDHVQIRLTELGTPTADLGLFQNEEDAKRYIRQLPQ 285
 DB 251 DVWVSGCIPMELNKRPLFGGRDHVQIRLTELGTPTADLGLFQNEEDAKRYIRQLPQ 309
 QY 286 HPRQOLAEEFPHVNPALIDLVKMLTFDPTRRITVEALRDHYLLAKHDAGDEPICVPV 345
 DB 310 HPRQSLPEKFFHVQPLAIDLVKMLTFDPRQITVEGALAHYLLASLHIDSEPGCSMPF 369
 QY 346 SPDFEEOGIGEOIKIMYOEALISNPEY 374
 DB 370 SDFEEOHALSEQMKDLIYOEALANPDY 398

RESULT 14
 Q9FSE6 PRELIMINARY; PRT; 369 AA.
 AC Q9FSE6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE MAPK2 protein.

GN MAPK2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Erihartoideae; Oryzaceae; Oryza.
 ON NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang H.J., Dai Y.H., Huang D.D., Kuo T.T.;
 RT "Molecular Cloning of a Low Temperature-Inducible MAP Kinase from
 RT Rice";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ250311; CAC13967.1;
 DR HSSP: Q16539; IMFC.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR AMP-binding; transferase.
 KW SEQUENCE 369 AA; 42957 MW; 1E7BF2603BAZFDB CRC64;
 SQ
 Query Match 74.1%; Score 1472; DB 10; Length 369;
 Best Local Similarity 72.2%; Pred. No. 1.1e-117;
 Matches 262; Conservative 58; Mismatches 43; Indels 0; Gaps 0;
 QY 10 GGCPDPFSSVLTGSGQYQDFDIFGNFEITTKYRPPIMPIGRGAYGIVCSVLTNEMV 69
 Db 3 GAVAEFRPTMTGGRILYIDFNKPEVTKYQPIPIRGGAYGIVCSVMTETRMV 62
 QY 70 AVKTIANAFDIYMDAKRTLRKILRLDHNENIGLRDVIPLRREFSDVYIATELMDT 129
 Db 63 AIKTIANAFNNDMAKRTLRKILRLDHNENIGLRDVIPLRREFSDVYIATELMDT 122
 QY 130 DLHGIINSNOGLSEDDHCQYFMYQLRGLKYHSANVLRDLKPSNLLVANCDLKICDFG 189
 Db 123 DLHIIINSNOGLSEDDHCQYFMYQLRGLKYHSANVLRDLKPSNLLVANCDLKICDFG 182
 QY 190 LARPNIENMTEYVYRWYRAPELLNNSDYTAIDVMSVGCIFMELNRRKPLFGKRDH 249
 Db 183 LARSSSDMTEYVYRWYRAPELLNNSDYTAIDVMSVGCIFMELNRRKPLFGKRDH 242
 QY 250 VHOIRLTTELLGTPEADGLFONEDAKRYIRQLPQHRQOLAEVPPHYNPLAIDLVDK 309
 Db 243 MHOIRLTTEVIGTPTDELGLFIRNEDAKRYIRQLPQHRQOLAEVPPHYNPLAIDLVDK 302
 QY 310 LTFDPRTITVEEALDHPYLAHLHDAGDEPICVPFSFDFBOGIGEBQIKMITYEALSLN 369
 Db 303 LTFNPLQRTITVEEALDHPYLAHLHDAGDEPICVPFSFDFBOGIGEBQIKMITYEAL 362
 QY 370 LNP 372
 Db 363 MNP 365
 RESULT 15
 Q9M534
 ID Q9M534 PRELIMINARY; PRT; 389 AA.
 AC Q9M534;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DE 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE Mitogen-activated protein kinase.
 OS Euphorbia esula (leafy spurge).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Malpighiales; Euphorbiaceae; Euphorbia.
 ON NCBI_Taxid=3993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-UNDERGROUND ADVENTITIOUS BUDS;
 RA Anderson J.V., Horvath D.P.;
 RT "Identification of mRNAs expressed in underground adventitious buds of
 RT Euphorbia esula (leafy spurge).";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF242308; AF65766.1;
 DR HSSP: P24941; IHCL.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003527; MAP_kin.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS01351; MAPK; UNKNOWN_1.
 DR PROSITE: PS0107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR AMP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW SEQUENCE 389 AA; 44697 MW; 7AC5BB570BB636E2 CRC64;
 SQ
 Query Match 74.1%; Score 1471.5; DB 10; Length 389;
 Best Local Similarity 75.0%; Pred. No. 1.3e-117;
 Matches 270; Conservative 43; Mismatches 46; Indels 1; Gaps 1;
 QY 15 DFPVSLTHGQYQDFDIFGNFEITTKYRPPIMPIGRGAYGIVCSVLTNEMVAYKKI 74
 Db 28 NIPATLSGGRFIQYNLFGNIFETAKYRPPIMPIGRGAYGIVCSVLTNEMVAYKKI 87
 QY 75 ANAFDIYMDAKRTLRKILRLDHNENIGLRDVIPLRREFSDVYIATELMDTLHQI 134
 Db 88 ANAFDNKIDAKRTLRKILRLDHNENIGLRDVIPLRREFSDVYIATELMDTLHQI 147
 QY 135 IRSNGLSEDDHCQYFMYQLRGLKYHSANVLRDLKPSNLLVANCDLKICDFGLARP 194
 Db 148 IRSNOALSEDDHCQYFMYQLRGLKYHSANVLRDLKPSNLLVANCDLKICDFGLARP 207
 QY 195 IENNMTEYVYRWYRAPELLNNSDYTAIDVMSVGCIFMELNRRKPLFGKRDH 254
 Db 208 SETPMTEYVYRWYRAPELLNNSDYTAIDVMSVGCIFMELNRRKPLFGKRDH 267
 QY 255 LTFELTGTPEADGLFONEDAKRYIRQLPQHRQOLAEVPPHYNPLAIDLVDKMLTFDP 314
 Db 268 LFMELIGPSEEDGLFONEDAKRYIRQLPQHRQOLAEVPPHYNPLAIDLVDKMLTFDP 326
 QY 315 TRRTITVEEALDHPYLAHLHDAGDEPICVPFSFDFBOGIGEBQIKMITYEALSLN 374
 Db 327 RQRTITVEEALDHPYLAHLHDAGDEPICVPFSFDFBOGIGEBQIKMITYEALSLN 386
 Search completed: May 20, 2003, 00:23:34
 Job time : 62 secs

GenCore version 5.1.5
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OM protein - protein search, using sw model

Run on: May 20, 2003, 00:20:45 ; Search time 35 seconds
(without alignments)
315.246 Million cell updates/sec

Title: US-09-623-034-2
Perfect score: 1987
Sequence: 1 MADANMGAGCGGPPDPFSLV.....EEQIKDMIVQDALSLNPEYA 375

Scoring table:
BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_patents_AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1987	100.0	375	2	US-08-837-593-5
2	1661	83.6	370	2	US-08-837-593-7
3	1634	82.2	371	2	US-08-837-593-6
4	1509	75.9	393	2	US-08-837-593-3
5	1500.5	75.5	387	2	US-08-837-593-4
6	1482	74.6	393	2	US-08-837-593-2
7	1292	65.0	371	2	US-08-837-593-8
8	1094.5	55.1	372	2	US-08-837-593-9
9	950	47.8	304	4	US-09-739-455-13
10	950	47.8	304	4	US-09-739-455-23
11	886.5	44.6	380	3	US-08-459-953A-9
12	885.5	44.6	415	1	US-08-176-620A-4
13	885.5	44.6	415	1	US-08-463-862-4
14	885.5	44.6	415	2	US-08-461-985-4
15	885.5	44.6	415	2	US-08-458-887-4
16	885.5	44.6	415	4	US-08-932-787B-4
17	885.5	44.6	415	4	US-08-932-012C-4
18	885.5	44.6	415	4	US-08-888-818C-4
19	878.5	44.2	360	4	US-09-457-040B-3
20	878.5	44.2	365	1	US-08-176-620A-2
21	878.5	44.2	365	1	US-08-463-862-2
22	878.5	44.2	365	2	US-08-461-985-2
23	878.5	44.2	365	2	US-08-458-887-2
24	878.5	44.2	365	4	US-08-932-787B-2
25	878.5	44.2	365	4	US-08-932-012C-2
26	878.5	44.2	365	4	US-08-888-818C-2
27	878.5	44.2	367	1	US-08-176-620A-11

28	878.5	44.2	367	2	US-08-461-985-11	Sequence 11, Appl
29	877.5	44.2	358	1	US-08-176-620A-12	Sequence 12, Appl
30	877.5	44.2	358	2	US-08-461-985-12	Sequence 12, Appl
31	877.5	44.2	358	4	US-09-457-040B-4	Sequence 4, Appl1
32	877.5	44.2	360	3	US-08-622-277A-14	Sequence 14, Appl
33	877.5	44.2	364	4	US-09-457-040B-34	Sequence 34, Appl
34	872	43.9	379	4	US-09-411-628-14	Sequence 14, Appl
35	870	43.8	353	1	US-08-176-620A-14	Sequence 14, Appl
36	870	43.8	353	2	US-08-461-985-14	Sequence 14, Appl
37	867	43.6	379	4	US-09-025-580-25	Sequence 25, Appl1
38	864.5	43.5	355	3	US-08-459-953A-8	Sequence 8, Appl1
39	864.5	43.5	365	4	US-09-457-040B-35	Sequence 35, Appl1
40	863.5	43.5	360	4	US-09-025-580-2	Sequence 2, Appl1
41	860	43.3	379	3	US-08-622-277A-8	Sequence 8, Appl1
42	849	42.7	353	4	US-08-932-787B-19	Sequence 19, Appl
43	849	42.7	353	4	US-08-932-012C-19	Sequence 19, Appl
44	849	42.7	353	4	US-08-888-818C-19	Sequence 19, Appl
45	841	42.3	360	1	US-08-674-612-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-837-593-5
; Sequence 5, Application US/08837593
; Patent No. 5977442
; GENERAL INFORMATION:
; APPLICANT: Kleesig, Daniel F.
; APPLICANT: Zhang Zhunqun
; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
; NUMBER OF SEQUENCES: 14
; CORESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
; ADDRESS: P. C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/837,593
; FILING DATE: April 21, 1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/029,805
; FILING DATE: October 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Janet E.
; REGISTRATION NUMBER: 36,252
; REFERENCE/DOCKET NUMBER: Rutgers 97-0016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; TELE: 563-4044
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 375 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-837-593-5

Query Match 100.0%; Score 1987; DB 2; Length 375;
 Best Local Similarity 100.0%; Pred. No. 1.2e-200;
 Matches 375; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MADANMGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKRPPIMPICRGAYGIVCSV 60
 DB 1 MADANMGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKRPPIMPICRGAYGIVCSV 60
 QY 61 LNTLNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDV 120
 DB 61 LNTLNMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDV 120
 QY 121 YIATLMDTDLHOIIRSNOSLSEDCQYFMVQLRLGLKXIHSAVNLHRDLKPSNLVYAN 180
 DB 121 YIATLMDTDLHOIIRSNOSLSEDCQYFMVQLRLGLKXIHSAVNLHRDLKPSNLVYAN 180
 QY 181 CDKICDGLARPIENENMTYVYTRAPPELLNNSDYTAIDVWSGCIPELMNR 240
 DB 181 CDKICDGLARPIENENMTYVYTRAPPELLNNSDYTAIDVWSGCIPELMNR 240
 QY 241 KPLFGGDHVOIRLLELTPTADLGFIONEDAKRYIRQLPQHPROQLAEVPHVNP 300
 DB 241 KPLFGGDHVOIRLLELTPTADLGFIONEDAKRYIRQLPQHPROQLAEVPHVNP 300
 QY 301 LAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIK 360
 DB 301 LAIDLVDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIK 360
 QY 361 DMVIOEALSLNPEYA 375
 DB 361 DMVIOEALSLNPEYA 375

RESULT 2

US-08-837-593-7

; Sequence 7, Application US/08837593
 ; Patent No. 5977442

; GENERAL INFORMATION:

; APPLICANT: Klessig, Daniel F.

; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced

; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,

; ADDRESSEE: P.C.

; STREET: 1601 Market Street, Suite 720

; CITY: Philadelphia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19103-2307

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/837,593

; FILING DATE: April 21, 1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/039,805

; FILING DATE: October 25, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Reed, Janet E.

; REGISTRATION NUMBER: 36,252

; REFERENCE/DOCKET NUMBER: Rutgers 97-0016

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 563-4100

; TELEFAX: (215) 563-4044

; TELEX:

; INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

; LENGTH: 370 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHEICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: Internal

; ORIGINAL SOURCE:

; US-08-837-593-7

Query Match 83.6%; Score 1661; DB 2; Length 370;
 Best Local Similarity 82.4%; Pred. No. 2.4e-166;
 Matches 304; Conservative 36; Mismatches 29; Indels 0; Gaps 0;

QY 6 MGAGGCGPPDPFVSVLTHGGQYVQFDIFGNFEITTKRPPIMPICRGAYGIVCSVLTTEL 65
 DB 1 MNTGGGQYTFPAVDTHGGQYVQFDIFGNFEITTKRPPIMPICRGAYGIVCSVLTTEL 60
 QY 66 NEMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDVYATATE 125
 DB 61 NEMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENYIGLRVYIPPLRERSDVYATATE 120
 QY 126 LMDTDLHOIIRSNOSLSEDCQYFMVQLRLGLKXIHSAVNLHRDLKPSNLVYANCDLKI 185
 DB 121 LMDTDLHOIIRSNOSLSEDCQYFMVQLRLGLKXIHSAVNLHRDLKPSNLVYANCDLKI 180
 QY 186 CDGLARPIENENMTYVYTRAPPELLNNSDYTAIDVWSGCIPELMNRKPLFG 245
 DB 181 CDGLARPIENENMTYVYTRAPPELLNNSDYTAIDVWSGCIPELMNRKPLFG 240
 QY 246 GKDHVOIRLLELTPTADLGFIONEDAKRYIRQLPQHPROQLAEVPHVNPPLAIDL 305
 DB 241 GKDHVOIRLLELTPTADLGFIONEDAKRYIRQLPQHPROQLAEVPHVNPPLAIDL 300
 QY 306 VDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIKMDIXQ 365
 DB 301 VDKMLTFDPTRITVEALDHPYLAKLHDAGDEPICVPVPSFDEQOIGEBQIKMDIXQ 360
 QY 366 EALSLNPEY 374
 DB 361 EALSLNPEY 369

RESULT 3

US-08-837-593-6

; Sequence 6, Application US/08837593
 ; Patent No. 5977442

; GENERAL INFORMATION:

; APPLICANT: Klessig, Daniel F.

; TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced

; TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Dann, Dorfman, Herrell and Skillman,

; ADDRESSEE: P.C.

; STREET: 1601 Market Street, Suite 720

; CITY: Philadelphia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19103-2307

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: IBM Compatible

; SOFTWARE: FastSeq Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/837,593

; FILING DATE: April 21, 1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; INFORMATION FOR SEQ ID NO: 7:

APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-837-593-6

Query Match 82.2%; Score 1634; DB 2; Length 371;
Best Local Similarity 82.8%; Pred. No. 1.6e-163;
Matches 299; Conservative 38; Mismatches 24; Indels 0; Gaps 0;

QY 15 DEPSVLTGGOYVOPDIFGNFELITTKRPPIMPIGRGAYGIVSVLTNEMVAVKKI 74
DB 11 EFPAVOTHGGOYVQYVNGNLFEEVAKYRPPIMPIGRGAYGIVCSLTNETELVAVKKI 70
QY 75 ANAFDIYADAKRTLEIKLRHLHDEHNYIGLDVIRPPRRFSPVYATLMDTDLHQI 134
DB 71 ANAFDHNADAKRTLEIKLRHLHDEHNYIGLDVIRPPRRFNDVYITTELMDDLHQI 130
QY 135 IRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLKPSNLLVYANCDLKIDFGLARP 194
DB 131 IRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLKPSNLLVYANCDLKIDFGLARP 190
QY 195 IENEMTEYVYTRWYRAPELLNNSDYTAIDVWSVGCIFMELMANKKPLFGKDHVQIR 254
DB 191 IENEMTEYVYTRWYRAPELLNNSDYTAIDVWSVGCIFMELMANKKPLFGKDHVQIR 250
QY 255 LTELGLPTDADGLFONEDAKRYIRQLPQHRQOLAEVFPVHNPALDLVDKMLTDP 314
DB 251 LTELGLPTDADGLFONEDAKRYIRQLPQHRQOLAEVFPVHNPALDLVDKMLTDP 310
QY 315 TRRTVEALDHPYLAKLHDAGDEPICVPFSFDEOOGIGEEQIKDMITQALSNPEY 374
DB 311 TRRTVEALDHPYLAKLHDAGDEPICVPFSFDEOOGIGEEQIKDMITQALSNPEY 370
QY 375 A 375
DB 371 A 371

RESULT 4
US-08-837-593-3
Sequence 3, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.
TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
ADDRESS: P.C.
CITY: Philadelphia
STATE: PA
COUNTRY: United States of America

ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,593
FILING DATE: April 21, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,805
FILING DATE: October 25, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Janet E.
REGISTRATION NUMBER: 36,252
REFERENCE/DOCKET NUMBER: Rutgers 97-0016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-837-593-3

Query Match 75.9%; Score 1509; DB 2; Length 393;
Best Local Similarity 72.6%; Pred. No. 2.5e-150;
Matches 278; Conservative 44; Mismatches 49; Indels 12; Gaps 2;

QY 3 DANMAGGGGFP-----DEPSVLTGGOYVOPDIFGNFELITTKRPPIMPICR 51
DB 9 DTVMSDAAQOPAPPSQYAGIDNIPATLSHGREFLYVIFGNIEVYAKYRPPIMPICR 68
QY 52 GAYGIVCSVLTNEMVAVKKIYANAFDIYADAKRTLEIKLRHLHDEHNYIGLDVIRPP 111
DB 69 GAYGIVCSVLTNEMVAVKKIYANAFDIYADAKRTLEIKLRHLHDEHNYIGLDVIRPP 128
QY 112 PLRREFSDVYATLMDTDLHQIIRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLK 171
DB 129 PLRREFSDVYATLMDTDLHQIIRSNOGLSEDCQYPMYOLLRLGLKYIHSANVLHRDLK 188
QY 172 PSNLLVYANCDLKIDFGLARPNIENEMTEYVYTRWYRAPELLNNSDYTAIDVWSVG 231
DB 189 PSNLLVYANCDLKIDFGLARPNIENEMTEYVYTRWYRAPELLNNSDYTAIDVWSVG 248
QY 232 CIFMELMANKKPLFGKDHVQIRLTELGLPTDADGLFONEDAKRYIRQLPQHRQOL 291
DB 249 CIFMELMANKKPLFGKDHVQIRLTELGLPTDADGLFONEDAKRYIRQLPQHRQOL 307
QY 292 AEVFPVHNPALDLVDKMLTFDPTTRITVEALDHPYLAKLHDAGDEPICVPFSFDEO 351
DB 308 AEVFPVHNPALDLVDKMLTFDPTTRITVEALDHPYLAKLHDAGDEPICVPFSFDEO 367
QY 352 OGIGEEQIKDMITQALSNPEY 374
DB 368 HALTEQMKELIYREGLAENPEY 390

RESULT 5
US-08-837-593-4
Sequence 4, Application US/08837593
Patent No. 5977442
GENERAL INFORMATION:
APPLICANT: Klessig, Daniel F.

```

? APPLICANT: Zhang Zhugun
? TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
? TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in Plant
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
? ADDRESSEE: P.C.
? STREET: 1601 Market Street, Suite 720
? CITY: Philadelphia
? STATE: PA
? COUNTRY: United States of America
? ZIP: 19103-2307
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/837,593
? FILING DATE: April 21, 1997
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/029,805
? FILING DATE: October 25, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Reed, Janet E.
? REGISTRATION NUMBER: 36,252
? REFERENCE/DOCKET NUMBER: Rutgers 97-0016
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 563-4100
? TELEFAX: (215) 563-4044
? TELEX:
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 387 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE: Internal
? ORIGINAL SOURCE:
?
US-08-837-593-4

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Query Match 75.5%; Score 1500.5; DB 2; Length 387;
Best Local Similarity 74.3%; Pred. No. 1.9e-149;
Matches 278; Conservative 43; Mismatches 52; Indels 1; Gaps 1;

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```

QY 1 MADANMAGGQPPDFPSVLTHGGQYQVDFIFGFEITTKYRPPIMPICGAYICSV 60
DB 13 MSDAAPAPQMGJENIPAVLSHGGRFIOYNIFGFEVTAKKPIMPICGAYICSA 72
QY 61 LNFELNEMVAVKRIANAFDIYMDAKRTLREIKLRHLDHENVAGLRDVIPIPLRRESDV 120
DB 73 HNSTETNHAVAKRIANAFDNKIDAKRTLREIKLRHMDHENVAVAKRIIVPPORRENFND 132
QY 121 YIATELMDTDLHQIIRSNQGLSEDHCOYFMQQLRGKLYHSANVLRDLKPSMLNVAN 180
DB 133 YIAELMDTDLHQIIRSNQGLSEHCOYFLYQILRGKLYHSANVLRDLKPSMLLNAN 192
QY 181 CDLKICQFGLARPNIEENMTEYVVTWRYRAPPELLNSSDYTAIDVWSGCIFFMELMR 240
DB 193 CDLKICQFGLARPNIEENMTEYVVTWRYRAPPELLNSSDYTAIDVWSGCIFFMELMR 252
QY 241 KPLGGGDHVOHRLTLELLGTPEADLGLQNEADAKRYRQLPQHRRQQLAEFFRVNP 300
DB 253 KPLPGGDHVOHRLTLELLGTPEADLGLQNEADAKRYRQLPQHRRQQLAEFFRVNP 311
QY 301 LAIDLVMKMLTFDPTRITVEEALDHPYLAKLHDAGDEPICVPFSEDFEQOGIGEQIK 360
DB 312 EALDVMKMLTFDPTRITVEEALDHPYLAKLHDAGDEPICVPFSEDFEQOGIGEQIK 371

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QY 361 DMIVQALSLNPEX 374
DB 372 ELIYREALAFNPEX 385

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```

RESULT 6
US-08-837-593-2
? Sequence 2, Application US/08837593
? Patent No. 5977442
? GENERAL INFORMATION:
? APPLICANT: Klesio, Daniel F.
? APPLICANT: Zhang Zhugun
? TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
? TITLE OF INVENTION: Map Kinase and its Use for Enhanced Disease Resistance in P
? NUMBER OF SEQUENCES: 14
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
? ADDRESSEE: P.C.
? STREET: 1601 Market Street, Suite 720
? CITY: Philadelphia
? STATE: PA
? COUNTRY: United States of America
? ZIP: 19103-2307
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette
? COMPUTER: IBM Compatible
? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq Version 1.5
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/837,593
? FILING DATE: April 21, 1997
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/029,805
? FILING DATE: October 25, 1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Reed, Janet E.
? REGISTRATION NUMBER: 36,252
? REFERENCE/DOCKET NUMBER: Rutgers 97-0016
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 563-4100
? TELEFAX: (215) 563-4044
? TELEX:
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 393 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEICAL: YES
? ANTI-SENSE: NO
? FRAGMENT TYPE: Internal
? ORIGINAL SOURCE:
?
US-08-837-593-2

```

```

Query Match 74.6%; Score 1482; DB 2; Length 393;
Best Local Similarity 71.5%; Pred. No. 1.7e-147;
Matches 274; Conservative 46; Mismatches 51; Indels 12; Gaps 2;

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```

QY 3 DANMAGGQPP-----DFPSVLTHGGQYQVDFIFGFEITTKYRPPIMPICR 51
DB 9 DYMSDAGARQPPAPQVAGMDNIPATLSHGGRFIOYNIFGFEVTAKKPIMPICR 68
QY 52 GAVGIVCSVNTLELNVAVAKRIANAFDIYMDAKRTLREIKLRHLDHENVAGLRDVIPI 111
DB 69 GAVGIVCSALNSETIEVAVAKRIANAFDNKIDAKRTLREIKLRHMDHENVAVAKRIIV 128
QY 112 PLRFEESDYIATELMDTDLHQIIRSNQGLSEDHCOYFMQQLRGKLYHSANVLRDLK 171
DB 129 PORAFAFDYIATELMDTDLHQIIRSNQGLSEHCOYFLYQILRGKLYHSANVLRDLK 188
QY 172 PSNLLVANCDLKICQFGLARPNIEENMTEYVVTWRYRAPPELLNSSDYTAIDVWSG 231

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[illegible]

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Db      10 ELKQIPTHEGKVEYNNVLGNFFEVTSKTIPIPIQPYGRGAYGMWCATSNSEKKEEPAIKKI 69
Qy      75 ANAFDIYDAKRTLEFEIKLRHLHDHENYIGLRDVIIPPLRREFSVDVIATELMDTLHOI 134
      70 GNAPFNRIADKRTLEIKELLSHMDHENIITIKIDIVRPDPREEFNVDYIYVELIMDTDLHOI 129
Qy      135 IFSNGLSDEHCOYVMYQGLRGLKYIHSANYLHRPLKFSNLLVYANCDLKITCDGLAPN 194
Db      130 IFSQALTDHDCQYIYLYQLLRGLKYVHSANVLHRPLKFSNLLVYANCDLKITCDGLATTT 189
Qy      195 IENEMATEYVYVYRWYRAPELLLNSSDYTAALDVMWSVGCIFMELNMRKPLFGSKDQVHOIR 254
Db      190 SEADPMTEYVYVYRWYRAPELLLNCTEYTAALDVMWSVGCIFMELNMRKPLFGSKDQVHOIR 249
Qy      255 LTELGLPTTEADLGLONEDAKRIIRQLPQHPROQLAEVPPHNPALIDYDKMLTFDP 314
Db      250 LIALGLSEDSDELGLFSNDARKYVKHLPRVPRHPFSQKPPDVSPLALDLAEERLVYFDP 309
Qy      315 TRRIVERALDHPYLAKLHDAGDEPFCVPFSPFDEQOGIEEOIKMDIYOEALSLNP 372
Db      310 AKRIVEALNHPFLISHREINBPVCDSPFNFDQASLSBDIKELIMNALKFDP 367

RESULT 8
US-08-837-593-9
: Sequence 9, Application US/08837593
: Patent No. 5977442
: GENERAL INFORMATION:
: APPLICANT: Klessig, Daniel F.
: APPLICANT: Zhang Zhunqun
: TITLE OF INVENTION: "No. 5977442el Salicylic Acid Induced
: TITLE OF INVENTION: Map Kinase and its use for Enhanced Disease Resistance in P
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dann, Dorfman, Herrell and Skillman,
: ADDRESSEE: P.C.
: STREET: 1601 Market Street, Suite 720
: CITY: Philadelphia
: STATE: PA
: COUNTRY: United States of America
: ZIP: 19103-2307
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837,593
: FILING DATE: April 21, 1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/029,805
: FILING DATE: October 25, 1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Janet E.
: REGISTRATION NUMBER: 36,252
: REFERENCE/DOCKET NUMBER: Rutgers 97-0016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 563-4100
: TELEFAX: (215) 563-4044
: TELEX:
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 372 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: Protein
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
: US-08-837-593-9

```



```
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,953A
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/029,494
FILING DATE: March 19, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Maiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/267
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 9 :
SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-953A-9
```

```
Query Match 44.6%; Score 886.5; DB 3; Length 380;
Best Local Similarity 46.5%; Pred.No.7,1e-85;
Matches 174; Conservative 73; Mismatches 114; Indels 13; Gaps 7;
```

```
QY 7 GAGGQGFDFPSVLTGG--QYVQDFDIGNFPEITTKYRPPIMPGRGAYGVCSVLNTE 64
DB 12 GGGGGPAAAMMAAAAGAPEVNR---QGVFDGPRY-TNLSYIEGAYGVCSAYDNV 66
QY 65 LNEAVAKIANAFDIYMDAKRTREIKLLRLDHEENVIGLRDVIIPPLRREFSDVIAT 124
DB 67 NKVRAIAIKI-SPEFHQYTCQRTLEIKLLRFHHENIIGIIDIIQAPRTIEQMKDYIYQ 125
QY 125 ELMDTDLHQIIRSNQGLSEDCQYFMYQLRGKLYIHSANVLRDLKPSNLLVNAKDIK 184
DB 126 DLMETDLKYLKLT-OHLSNDHICFLYQILRGKLYIHSANVLRDLKPSNLLNTCDLK 184
QY 185 ICDPEFLAR---PNIENEN-MTEYVYTRMYRAPPELLNNSDYTAADWVSGCFMELMRK 240
DB 185 ICDPEFLARADDDHDTGFLTEYVATRWYRAPEIMLNSGYKSIDWVSGCI LAEMLSN 244
QY 241 KPLFGKDHVHQIRLTTELGTPTTEADLGFQNEADAKRYIRQLPQHPROQLAEVPPHVP 300
DB 245 RPIFGKHYLDQNLHILGLISPSQEDLNCITNLKARNLTLSPHKNKYPMWRLEFPNADS 304
QY 301 LAIDLVDKMLTFDPTRRITVEBALDHPYLAKLHDAGDEPICVPSPFDEQOIGEEQIK 360
DB 305 KALDLDKMLTFNPHKRIEVEQALAHPLYLEQYDPSDEPIAEAPKFDWELDLDPKELK 364
QY 361 DMIVQEALSLNPEY 374
DB 365 ELIFEETARFOPGY 378
```

```
RESULT 12
US-08-176-620A-4
Sequence 4, Application US/08176620A
Patent No. 5595904
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G.
APPLICANT: Cobb, Melanie H.
APPLICANT: Yancopoulos, George D.
APPLICANT: Nye, Steven
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A Family of Map2 Protein Kinases
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
```

```
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/176,620A
FILING DATE: 03-JAN-1994
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4 :
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-176-620A-4
```

```
Query Match 44.6%; Score 885.5; DB 1; Length 415;
Best Local Similarity 46.8%; Pred.No.1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;
```

```
QY 9 GGGQPPDFPSVLTTHGGVQDFDIGNFPEITTKYRPPIMPGRGAYGVCSVLNTELMEM 68
DB 51 GGGCAAMMAAAAGAPEVNR----QGVFDGPRY-TNLSYIEGAYGVCSAYDNVKNR 105
QY 69 YAVKRIANAFDIYMDAKRTREIKLLRLDHEENVIGLRDVIIPPLRREFSDVIATLMD 128
DB 106 VAIKKI-SPEFHQYTCQRTLEIKLLRFHHENIIGIIDIIQAPRTIEQMKDYIYQDLE 164
QY 129 TDLHQIIRSNQGLSEDCQYFMYQLRGKLYIHSANVLRDLKPSNLLVNAKDIKIDCF 188
DB 165 TDLVYLKLT-OHLSNDHICFLYQILRGKLYIHSANVLRDLKPSNLLNTCDLKICDF 223
QY 189 GLAR---PNIENEN-MTEYVYTRMYRAPPELLNNSDYTAADWVSGCFMELMRKPL 244
DB 224 GLARVADDDHDTGFLTEYVATRWYRAPEIMLNSGYKSIDWVSGCI LAEMLSNRLP 283
QY 245 GSKDENVHQIRLTTELGTPTTEADLGFQNEADAKRYIRQLPQHPROQLAEVPPHVP 304
DB 284 PEKHYLDQNLHILGLISPSQEDLNCITNLKARNLTLSPHKNKYPMWRLEFPNADSKALD 343
QY 305 LVDKMLTFDPTRRITVEBALDHPYLAKLHDAGDEPICVPSPFDEQOIGEEQIKDMY 364
DB 344 LLDKMLTFNPHKRIEVEQALAHPLYLEQYDPSDEPIAEAPKFDWELDLDPKELKELIF 403
QY 365 QEALSLNPEY 374
DB 404 EETARFOPGY 413
```

```
RESULT 13
US-08-463-862-4
Sequence 4, Application US/08463862
Patent No. 5776751
GENERAL INFORMATION:
APPLICANT: Boulton, Teri G. et al.
APPLICANT: Panayotatos, Nikos
TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
```


Search completed: May 20, 2003, 00:25:17
Job time : 36 secs

```
; Sequence 4, Application US/08458887
; Patent No.: 5914261
; GENERAL INFORMATION:
; APPLICANT: Boulton, Teri G. et al.
; TITLE OF INVENTION: A FAMILY OF MAP2 PROTEIN KINASES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,887
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,544
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 415 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-887-4
```

```
Query Match 44.6%; Score 885.5; DB 2; Length 415;
Best Local Similarity 46.8%; Pred. No. 1e-84;
Matches 173; Conservative 73; Mismatches 113; Indels 11; Gaps 6;

QY 9 GGGGPPDPSPVLTGGGVYQFDIFGNFEITTKYRPPIMPICRGAYICVSVLNTLELME 68
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 51 GGGCANMAAAAAAGPEVNR--GQVFDVGPY-TNLSYIGEGAYGMVCSAYDMLNKYR 105
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 69 VAVKRIANAFDIYMDAKRTLRREIKLRLHDHENVIGLRDVIPPLRREFSDVYIATELMD 128
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 VAIKRI-SPEHQYTCQRTLRREIKLRLFRHNIIGINDIIRAPLIEQMKDYIYVDLME 164
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 129 TDLHOIIRSNQGLFEDHCQYFYQLRGIKYHSANVLHRLDKPSNLLVANCCLKICDF 188
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 165 TDLVYKLLKT-OHLSDNHICYFLYQILRGIKYHSANVLHRLDKPSNLLNTCTCLKICDF 223
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 189 GLAR--PIENEN-MTEYVYTRBWRAPPELLNSSDYTAIDVMSVGCIFMELMNRKPLF 244
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 224 GLARVADPDHDTGFTLEVATRWTRAPELMNSKGYTKSIDVMSVGCILAEMLSNRPLF 283
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 245 GKKDHVHQLRLTELLGTPTTEADLGLTQNEADAKRYIRQLPQHPROOLAEPFPHVNPPLAID 304
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 284 PKHVLDTQNLNHLIGLISPSQEDLNCIINLKARNYLLSLPHKNKYPMWNRLLFPNADSKALD 343
   || : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 305 LVDKMLTFDPTRRTIVEEALDHPYLAKLHDAGDEPICVPYPSFDFEQGIGEEQIKDMTY 364
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 LLDKMLTFNPNKRIRIVEQALAPLYEYDPSDEPIAEAPFKFDWELDLPEKELKELIF 403
   |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 365 QEALSLNPEY 374
   :| :
Db 404 EETARFQPGY 413
```

